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(54) Title: METHOD FOR STABLE CHROMOSOMAL MULTI-COPY INTEGRATION OF GENES

(57) Abstract: The present invention solves the problem of integrating multiple copies of a gene of interest by homologous recom-  
bination into well defined positions adjacent to conditionally essential genes in a bacterial host strain chromosome, which already  
comprises at least one copy of the gene of interest in a different position.

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**Method for stable chromosomal multi-copy integration of genes****Field of the Invention**

The invention relates to a method for inserting genes  
5 into the chromosome of bacterial strains, and the resulting  
strains. In the biotech industry it is desirable to construct  
polypeptide production strains having several copies of a gene  
of interest stably chromosomally integrated, without leaving  
antibiotic resistance marker genes in the strains.

10

**Background of the Invention**

In the industrial production of polypeptides it is of  
interest to achieve a product yield as high as possible. One  
way to increase the yield is to increase the copy number of a  
15 gene encoding a polypeptide of interest. This can be done by  
placing the gene on a high copy number plasmid, however  
plasmids are unstable and are often lost from the host cells  
if there is no selective pressure during the cultivation of  
the host cells. Another way to increase the copy number of the  
20 gene of interest is to integrate it into the host cell  
chromosome in multiple copies. It has previously been  
described how to integrate a gene into the chromosome by  
double homologous recombination without using antibiotic  
markers (Hone et al., Microbial Pathogenesis, 1988, 5: 407-  
25 418); integration of two genes has also been described (Novo  
Nordisk: WO 91/09129 and WO 94/14968). A problem with  
integrating several copies of a gene into the chromosome of a  
host cell is instability. Due to the sequence identity of the  
copies there is a high tendency for the them to recombine out  
30 of the chromosome again during cultivation of the host cell  
unless a selective marker or other essential DNA is included  
between the copies and selective pressure is applied during  
cultivation, especially if the genes are located in relative  
close vicinity of each other. It has been described how to

integrate two genes closely spaced in anti-parallel tandem to achieve better stability (Novo Nordisk: WO 99/41358).

The present day public debate concerning the industrial use of recombinant DNA technology has raised some questions  
5 and concern about the use of antibiotic marker genes. Antibiotic marker genes are traditionally used as a means to select for strains carrying multiple copies of both the marker genes and an accompanying expression cassette coding for a polypeptide of industrial interest. In order to comply with  
10 the current demand for recombinant production host strains devoid of antibiotic markers, we have looked for possible alternatives to the present technology that will allow substitution of the antibiotic markers we use today with non-antibiotic marker genes. Thus in order to provide recombinant  
15 production strains devoid of antibiotic resistance markers, it remains of industrial interest to find new methods to stably integrate genes in multiple copies into host cell chromosomes.

#### **Summary of the Invention**

20 The present invention solves the problem of integrating multiple copies of a gene of interest by homologous recombination into well defined chromosomal positions of a bacterial host strain which already comprises at least one copy of the gene of interest in a different position. This can  
25 be done by making a deletion of part of one or more conditionally essential gene(s) (hereafter called the "integration gene") in the host chromosome of a strain which already comprises at least one copy of a gene of interest, or by otherwise altering the gene(s) to render it non-functional;  
30 or by integrating at least one partial non-functional conditionally essential gene into the host chromosome, so that the resulting strain has a deficiency (e.g. specific carbon-source utilization) or a growth requirement (e.g. amino acid

auxotrophy) or is sensitive to a given stress. The next (i.e. second or third etc.) copy of the gene of interest is then introduced on a vector, on which the gene is flanked upstream by a partial fragment of the integration gene, and downstream 5 is flanked by a fragment homologous to a DNA sequence downstream of the integration gene on the host chromosome. Thus, neither host chromosome nor the incoming vector contain a full version of the integration gene. In a non-limiting example the host chromosome may comprise the first two thirds 10 of the integration gene and the vector the last two thirds, effectively establishing a sequence overlap of one third of the integration gene on the vector and the chromosome.

Expression of the full version of the integration gene will only occur if homologous recombination between vector and 15 host chromosome takes place via the partial integration gene sequences, and this particular recombination event can be efficiently selected for, even against the background of homologous integration into the chromosome directed by the gene of interest into the identical gene(s) comprised on the 20 chromosome already.

This strategy will enable directed gene integration by homologous recombination at predetermined loci, even though extended homology exists between the gene of interest on the incoming vector and other copies of this gene at other 25 locations in the chromosome, and even though it is not feasible to identify the desired integrants based on the qualitative phenotype resulting from expression of the gene of interest, as this gene is already present in one or more copies in the host.

30 In a non-limiting example herein a *Bacillus* enzyme production strain is provided that comprises two anti-parallel copies (inverted orientation) of a gene encoding the commercially available amylase Termamyl® (Novo Nordisk,

Denmark). A gene homologous to the *dal* gene of *Bacillus subtilis*, encoding a D-alanine racemase, was identified in the *Bacillus* production strain, it was sequenced and a partial deletion was made in the *dal* gene of the *Bacillus* two-copy  
5 Termamyl<sup>®</sup> strain. A vector was constructed to effect a stable non-tandem chromosomal insertion of a third Termamyl<sup>®</sup> gene copy adjacent to the *dal* locus, in the process effectively restoring the complete *dal* gene, according to the above strategy.

10 In another non-limiting example herein, an additional copy of the amylase encoding gene was introduced into the xylose isomerase operon of the *Bacillus* enzyme production strain which already comprised at least two copies of the amylase gene located elsewhere on the chromosome.

15 Also in a non-limiting example we demonstrate the method of the invention by integrating an additional amylase-encoding gene into the gluconat operon of the *Bacillus* enzyme production strain. Other non-limiting examples of integration into conditionally essential genes are given below.

20 Accordingly in a first aspect the invention relates to a method for constructing a cell comprising at least two copies of a gene of interest stably integrated into the chromosome in different positions, the method comprising the steps of:

- a) providing a host cell comprising at least one chromosomal  
25 copy of the gene of interest, and comprising one or more conditionally essential chromosomal gene(s) which has been altered to render the gene(s) non-functional;
- b) providing a DNA construct comprising:
  - i) an altered non-functional copy of the conditionally  
30 essential gene(s) of step a); and
  - ii) at least one copy of the gene of interest flanked on one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence located on the

- host cell chromosome adjacent to the gene(s) of step a); wherein a first recombination between the altered copy of i) and the altered chromosomal gene(s) of step a) restores the conditionally essential chromosomal gene(s) to functionality and renders the cell selectable;
- 5 to functionality and renders the cell selectable;
- c) introducing the DNA construct into the host cell and cultivating the cell under selective conditions that require a functional conditionally essential gene(s); and
- d) selecting a host cell that grows under the selective conditions of the previous step ; wherein the at least one copy of the gene of interest has integrated into the host cell chromosome adjacent to the gene(s) of step a); and optionally
- 10 conditions of the previous step ; wherein the at least one copy of the gene of interest has integrated into the host cell chromosome adjacent to the gene(s) of step a); and optionally
- e) repeating steps a) to d) at least once using a different chromosomal gene(s) in step a) in each repeat.
- 15 chromosomal gene(s) in step a) in each repeat.

- Another way of describing the first aspect of the invention relates to a method for constructing a cell comprising at least two copies of a gene of interest stably integrated into the chromosome in different positions, the method comprising the steps of:
- 20 integrated into the chromosome in different positions, the method comprising the steps of:
- a) providing a host cell comprising at least one chromosomal copy of the gene of interest;
- b) altering a conditionally essential chromosomal gene(s) of the host cell whereby the gene becomes non-functional;
- 25 the host cell whereby the gene becomes non-functional;
- c) making a DNA construct comprising:
- i) an altered non-functional copy of the chromosomal gene(s) of step b); and
- ii) at least one copy of the gene of interest flanked on one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence adjacent to the gene(s) of step b); wherein a first recombination between the altered copy of i) and the altered
- 30 one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence adjacent to the gene(s) of step b); wherein a first recombination between the altered copy of i) and the altered

chromosomal gene(s) of step b) restores the chromosomal gene(s) to functionality and renders the cell selectable;

- d) introducing the DNA construct into the host cell and  
5 cultivating the cell under selective conditions that require a functional gene(s) of step b); and  
e) selecting a host cell that grows under the selective conditions of step d); wherein the at least one copy of the gene of interest has integrated into the host cell  
10 chromosome adjacent to the gene(s) of step b); and optionally  
f) repeating steps a) to e) at least once using a different chromosomal gene(s) in step b) in each repeat.

Herein genetic tools are also described in the form of  
15 DNA constructs necessary for carrying out the method of the invention.

Consequently in a second aspect the invention relates to a DNA construct comprising:

- i) an altered non-functional copy of a conditionally  
20 essential chromosomal gene(s) from a host cell, preferably the copy is partially deleted; and  
ii) at least one copy of a gene of interest flanked on one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence located on the host  
25 cell chromosome adjacent to the conditionally essential gene(s) of i).

The present invention provides a method for obtaining a host cell comprising at least two copies of a gene of interest  
30 stably integrated on the chromosome adjacent to conditionally essential loci.

Accordingly in a third aspect the invention relates to a host cell comprising at least two copies of a gene of interest

stably integrated into the chromosome, where at least one copy is integrated adjacent to a conditionally essential locus and wherein the cell is obtainable by any of the methods defined in the first aspects.

5 Another way of describing an aspect of the invention relates to a host cell comprising at least two copies of a gene of interest stably integrated into the chromosome, where each copy is integrated adjacent to different conditionally essential loci and wherein the cell is obtainable by any of  
10 the methods defined in the first aspects.

The method of the invention relies on complementing a conditionally essential gene(s) that was rendered non-functional, and a number of suitable host cells comprising such non-functional genes are described herein. To carry out  
15 multiple rounds of gene integration according to the invention it is advantageous to provide a host cell comprising several non-functional conditionally essential genes.

In a fourth aspect the invention relates to a *Bacillus licheniformis* cell, wherein at least two conditionally  
20 essential genes are rendered non-functional, preferably the genes are chosen from the group consisting of *xylA*, *gale*, *gntK*, *gntP*, *glpP*, *glpF*, *glpK*, *glpD*, *araA*, *metC*, *lysA*, and *dal*.

Any host cell as described herein for use in a method of the invention is intended to be encompassed by the scope of  
25 the invention.

Another aspect of the invention relates to the use of a cell as defined in the previous aspect in a method as defined in the first aspects.

As mentioned above, genetic tools of the invention are  
30 described herein, and it is intended that the scope of the invention comprises such constructs when present in or propagated in host cells as is common in the art.

Yet another aspect of the invention relates to a cell comprising a DNA construct as defined in the second aspect.



In a final aspect the invention relates to a process for producing an enzyme of interest, comprising cultivating a cell as defined in any of the preceding aspects under conditions appropriate for producing the enzyme, and optionally purifying  
5 the enzyme.

### Figures

Figure 1: Schematic representation of the *B. licheniformis* xylose isomerase region, PCR fragments, Deletion  
10 and Integration plasmids and strains.

Figure 2: Schematic representation of the *B. licheniformis* gluconat region, PCR fragments, Deletion and Integration plasmids and strains.

Figure 3: Schematic representation of the *B. licheniformis* D-alanine racemase encoding region, PCR  
15 fragments, Deletion and Integration plasmids and strains.

### Definitions

In accordance with the present invention there may be  
20 employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory  
25 Press, Cold Spring Harbor, New York (herein "Sambrook et al., 1989") *DNA Cloning: A Practical Approach*, Volumes I and II /D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds (1985)); *Transcription And Translation* (B.D. Hames  
30 & S.J. Higgins, eds. (1984)); *Animal Cell Culture* (R.I. Freshney, ed. (1986)); *Immobilized Cells And Enzymes* (IRL Press, (1986)); B. Perbal, *A Practical Guide To Molecular Cloning* (1984).

A "polynucleotide" is a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases, the sequence of the polynucleotide is the actual sequence of the bases read from the 5' to the 3' end of the polymer.

5 Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic molecules.

A "nucleic acid molecule" or "nucleotide sequence" refers to the phosphate ester polymeric form of ribonucleosides  
10 (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine; "DNA molecules") in either single stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible.  
15 The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary or quaternary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear or circular DNA  
20 molecules (e.g., restriction fragments), plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of  
25 DNA (i.e., the strand having a sequence homologous to the mRNA). A "recombinant DNA molecule" is a DNA molecule that has undergone a molecular biological manipulation.

A DNA "coding sequence" or an "open reading frame (ORF)" is a double-stranded DNA sequence which is transcribed and  
30 translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The ORF "encodes" the polypeptide. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3'

(carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. If the coding sequence is  
5 intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

An expression vector is a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of  
10 interest operably linked to additional segments that provide for its transcription. Such additional segments may include promoter and terminator sequences, and optionally one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, and the like. Expression  
15 vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of  
20 a coding sequence in a host cell e.g. in eukaryotic cells, polyadenylation signals are control sequences.

A "secretory signal sequence" is a DNA sequence that encodes a polypeptide (a "secretory peptide" that, as a component of a larger polypeptide, directs the larger  
25 polypeptide through a secretory pathway of a cell in which it is synthesized. The larger polypeptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

The term "promoter" is used herein for its art-recognized  
30 meaning to denote a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

A chromosomal gene is rendered "non-functional" if the polypeptide that the gene encodes can no longer be expressed in a functional form. Such non-functionality of a gene can be induced by a wide variety of genetic manipulations or  
5 alterations as known in the art, some of which are described in Sambrook et al. *vide supra*. Partial deletions within the ORF of a gene will often render the gene non-functional, as will mutations e.g. substitutions, insertions, frameshifts etc.

10 "Operably linked", when referring to DNA segments, indicates that the segments are arranged so that they function in concert e.g. the transcription process takes place via the RNA-polymerase binding to the promoter segment and proceeding with the transcription through the coding segment until the  
15 polymerase stops when it encounters a transcription terminator segment.

"Heterologous" DNA in a host cell, in the present context refers to exogenous DNA not originating from the cell.

As used herein the term "nucleic acid construct" is  
20 intended to indicate any nucleic acid molecule of cDNA, genomic DNA, synthetic DNA or RNA origin. The term "construct" is intended to indicate a nucleic acid segment which may be single- or double-stranded, and which may be based on a complete or partial naturally occurring nucleotide sequence  
25 encoding a polypeptide of interest. The construct may optionally contain other nucleic acid segments.

The nucleic acid construct of the invention encoding the polypeptide of the invention may suitably be of genomic or cDNA origin, for instance obtained by preparing a genomic or  
30 cDNA library and screening for DNA sequences coding for all or part of the polypeptide by hybridization using synthetic oligonucleotide probes in accordance with standard techniques (cf. Sambrook et al., *supra*).

The nucleic acid construct of the invention encoding the polypeptide may also be prepared synthetically by established standard methods, e.g. the phosphoramidite method described by Beaucage and Caruthers, Tetrahedron Letters 22 (1981), 1859 - 5 1869, or the method described by Matthes et al., EMBO Journal 3 (1984), 801 - 805. According to the phosphoramidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in suitable vectors.

10 Furthermore, the nucleic acid construct may be of mixed synthetic and genomic, mixed synthetic and cDNA or mixed genomic and cDNA origin prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate), the fragments corresponding to various parts of the entire nucleic  
15 acid construct, in accordance with standard techniques. The nucleic acid construct may also be prepared by polymerase chain reaction using specific primers, for instance as described in US 4,683,202 or Saiki et al., Science 239 (1988), 487 - 491.

20 The term nucleic acid construct may be synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences necessary for expression of a coding sequence of the present invention

The term "control sequences" is defined herein to include  
25 all components that are necessary or advantageous for expression of the coding sequence of the nucleic acid sequence. Each control sequence may be native or foreign to the nucleic acid sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, a  
30 polyadenylation sequence, a propeptide sequence, a promoter, a signal sequence, and a transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of

introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleic acid sequence encoding a polypeptide.

The control sequence may be an appropriate promoter  
5 sequence, a nucleic acid sequence that is recognized by a host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences that mediate the expression of the polypeptide. The promoter may be any nucleic acid sequence  
10 that shows transcriptional activity in the host cell of choice and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

The control sequence may also be a suitable transcription  
15 terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleic acid sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present  
20 invention.

The control sequence may also be a polyadenylation sequence, a sequence which is operably linked to the 3' terminus of the nucleic acid sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine  
25 residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a signal peptide-coding region, which codes for an amino acid sequence linked to the  
30 amino terminus of the polypeptide which can direct the expressed polypeptide into the cell's secretory pathway of the host cell. The 5' end of the coding sequence of the nucleic acid sequence may inherently contain a signal peptide-coding region naturally linked in translation reading frame with the

segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide-coding region which is foreign to that portion of the coding sequence which encodes the secreted polypeptide. A foreign signal peptide-coding region may be required where the coding sequence does not normally contain a signal peptide-coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to obtain enhanced secretion of the polypeptide relative to the natural signal peptide coding region normally associated with the coding sequence. The signal peptide-coding region may be obtained from a glucoamylase or an amylase gene from an *Aspergillus* species, a lipase or proteinase gene from a *Rhizomucor* species, the gene for the alpha-factor from *Saccharomyces cerevisiae*, an amylase or a protease gene from a *Bacillus* species, or the calf preprochymosin gene. However, any signal peptide coding region capable of directing the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

The control sequence may also be a propeptide coding region, which codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the *Bacillus subtilis* alkaline protease gene (*aprE*), the *Bacillus subtilis* neutral protease gene (*nprT*), the *Saccharomyces cerevisiae* alpha-factor gene, or the *Myceliophthora thermophilum* laccase gene (WO 95/33836).

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the

polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory  
5 compound. Regulatory systems in prokaryotic systems would include the *lac*, *tac*, and *trp* operator systems. Other examples of regulatory sequences are those which allow for gene amplification. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the  
10 presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleic acid sequence encoding the polypeptide would be placed in tandem with the regulatory sequence.

Examples of suitable promoters for directing the  
15 transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli lac* operon, the *Streptomyces coelicolor* agarase gene (*dagA*), the *Bacillus subtilis* levansucrase gene (*sacB*), the *Bacillus subtilis*  
20 alkaline protease gene, the *Bacillus licheniformis* alpha-amylase gene (*amyL*), the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), the *Bacillus amyloliquefaciens* BAN AMYLASE GENE, the *Bacillus licheniformis* penicillinase gene  
25 (*penP*), the *Bacillus subtilis* *xylA* and *xylB* genes, and the prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, *Proceedings of the National Academy of Sciences USA* 75:3727-3731), as well as the *tac* promoter (DeBoer et al., 1983, *Proceedings of the National Academy of Sciences USA* 80:21-25).  
30 Further promoters are described in "Useful proteins from recombinant bacteria" in *Scientific American*, 1980, 242:74-94; and in Sambrook et al., 1989, *supra*.

The present invention also relates to recombinant expression vectors comprising a nucleic acid sequence of the



present invention, a promoter, and transcriptional and translational stop signals. The various nucleic acid and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleic acid sequence encoding the polypeptide at such sites. Alternatively, the nucleic acid sequence of the present invention may be expressed by inserting the nucleic acid sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression, and possibly secretion.

15 The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleic acid sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids. The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon.

The vectors of the present invention preferably contain one or more "selectable markers" which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide, antibiotic or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

A "conditionally essential gene" may function as a "non-antibiotic selectable marker". Non-limiting examples of bacterial conditionally essential selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, that are only essential when the bacterium is cultivated in the absence of D-alanine. Also the genes encoding enzymes involved in the turnover of UDP-galactose can function as conditionally essential markers in a cell when the cell is grown in the presence of galactose or grown in a medium which gives rise to the presence of galactose. Non-limiting examples of such genes are those from *B. subtilis* or *B. licheniformis* encoding UTP-dependent phosphorylase (EC 2.7.7.10), UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or UDP-galactose epimerase (EC 5.1.3.2). Also a xylose isomerase gene such as *xylA*, of *Bacilli* can be used as selectable markers in cells grown in minimal medium with xylose as sole carbon source. The genes necessary for utilizing gluconate, *gntK*, and *gntP* can also be used as selectable markers in cells grown in minimal medium with gluconate as sole carbon source. Other non-limiting examples of conditionally essential genes are given below.

Antibiotic selectable markers confer antibiotic resistance to such antibiotics as ampicillin, kanamycin, chloramphenicol, erythromycin, tetracycline, neomycin, hygromycin or methotrexate.

Furthermore, selection may be accomplished by co-transformation, e.g., as described in WO 91/17243, where the selectable marker is on a separate vector.

The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector, or of a smaller part of the vector, into the host cell genome or autonomous replication of the vector in the cell  
5 independent of the genome of the cell.

The vectors, or smaller parts of the vectors, may be integrated into the host cell genome when introduced into a host cell. For chromosomal integration, the vector may rely on the nucleic acid sequence encoding the polypeptide or any  
10 other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination.

Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous  
15 recombination into the genome of the host cell. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements  
20 should preferably contain a sufficient number of nucleic acids, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous  
25 recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleic acid sequences.

The copy number of a vector, an expression cassette, an  
30 amplification unit, a gene or indeed any defined nucleotide sequence is the number of identical copies that are present in a host cell at any time. A gene or another defined chromosomal nucleotide sequence may be present in one, two, or more copies

on the chromosome. An autonomously replicating vector may be present in one, or several hundred copies per host cell.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to  
5 replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, pACYC184, pUB110, pE194, pTA1060, and pAM $\beta$ 1. The origin of replication may be one having a mutation which makes its functioning  
10 temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, *Proceedings of the National Academy of Sciences USA* 75:1433).

The present invention also relates to recombinant host cells, comprising a nucleic acid sequence of the invention, which are  
15 advantageously used in the recombinant production of the polypeptides. The term "host cell" encompasses any progeny of a parent cell which is not identical to the parent cell due to mutations that occur during replication.

The cell is preferably transformed with a vector  
20 comprising a nucleic acid sequence of the invention followed by integration of the vector into the host chromosome. "Transformation" means introducing a vector comprising a nucleic acid sequence of the present invention into a host cell so that the vector is maintained as a chromosomal  
25 integrant or as a self-replicating extra-chromosomal vector. Integration is generally considered to be an advantage as the nucleic acid sequence is more likely to be stably maintained in the cell. Integration of the vector into the host chromosome may occur by homologous or non-homologous  
30 recombination as described above.

The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source. The host cell may be a unicellular microorganism, e.g., a prokaryote, or a non-unicellular microorganism, e.g., a

eukaryote. Useful unicellular cells are bacterial cells such as gram positive bacteria including, but not limited to, a *Bacillus* cell, e.g., *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*,  
5 *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*; or a *Streptomyces* cell, e.g., *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria  
10 such as *E. coli* and *Pseudomonas* sp. In a preferred embodiment, the bacterial host cell is a *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus stearothermophilus* or *Bacillus subtilis* cell.

The transformation of a bacterial host cell may, for  
15 instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Molecular General Genetics* 168:111-115), by using competent cells (see, e.g., Young and Spizizin, 1961, *Journal of Bacteriology* 81:823-829, or Dubnar and Davidoff-Abelson, 1971, *Journal of Molecular Biology* 56:209-  
20 221), by electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6:742-751), or by conjugation (see, e.g., Koehler and Thorne, 1987, *Journal of Bacteriology* 169:5771-5278).

The transformed or transfected host cells described above  
25 are cultured in a suitable nutrient medium under conditions permitting the expression of the desired polypeptide, after which the resulting polypeptide is recovered from the cells, or the culture broth.

The medium used to culture the cells may be any conventional  
30 medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared

using procedures known in the art (see, e.g., references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

If the polypeptide is secreted into the nutrient medium, 5 the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it is recovered from cell lysates. The polypeptide are recovered from the culture medium by conventional procedures including separating the host cells from the medium by centrifugation or filtration, precipitating 10 the proteinaceous components of the supernatant or filtrate by means of a salt, e.g. ammonium sulphate, purification by a variety of chromatographic procedures, e.g. ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like, dependent on the type of 15 polypeptide in question.

The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme 20 substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide.

The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, 25 hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing (IEF), differential solubility (e.g., ammonium sulfate precipitation), or extraction (see, e.g., *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH 30 Publishers, New York, 1989).

#### Detailed description of the invention

A method for constructing a cell comprising at least two copies of a gene of interest stably integrated into the

chromosome in different positions according to the first aspect of the invention.

In the method of the invention it is envisioned that after the directed and selectable integration of the DNA construct into the chromosome of the host cell by the first homologous recombination, a second recombination can take place between a DNA fragment comprised in the construct and a homologous host cell DNA sequence located adjacent to the gene(s) of step b) of the method of the first aspect, where  
10 the DNA fragment of the construct is homologous to said host cell DNA sequence.

Accordingly a preferred embodiment of the invention relates to the method of the first aspect, wherein subsequent to the step of introducing the DNA construct and cultivating  
15 the cell under selective conditions, or subsequent to the step of selecting a host cell, a second recombination takes place between the DNA fragment and the homologous host cell DNA sequence.

A preferred embodiment of the invention relates to the  
20 method of the first aspect, wherein subsequent to step d) and prior to step e) a second recombination takes place between the DNA fragment and the homologous host cell DNA sequence.

Further it is envisioned that one might add a marker gene to the DNA construct, which could ease selection of first  
25 recombination integrants, where the marker gene would be excised from the host cell chromosome again by the second recombination as described above.

In a preferred embodiment the invention relates to the method of the first aspect, where the DNA construct further  
30 comprises at least one marker gene which is located in the construct such that it is recombined out of the chromosome by the second recombination; preferably the at least one marker gene confers resistance to an antibiotic, more preferably the antibiotic is chosen from the group consisting of

chloramphenicol, kanamycin, ampicillin, erythromycin, spectinomycin and tetracycline; and most preferably a host cell is selected which grows under the selective conditions, and which does not contain the at least one marker gene in the 5 chromosome.

The method of the invention can also be carried out by including a marker gene in that part of the DNA construct which remains integrated in the chromosome after the second recombination event. However as it is preferred not to have 10 marker genes in the chromosome, an alternative way of removing the marker gene must be employed after the integration has been carried out. Specific restriction enzymes or resolvases that excise portions of DNA, if it is flanked on both sides by certain recognition sequences known as resolvase sites or *res-* 15 sites, are well known in the art, see e.g. WO 96/23073 (Novo Nordisk A/S) which is included herein by reference.

A preferred embodiment of the invention relates to the method of the first aspect, where the DNA construct further comprises at least one marker gene located between the altered 20 copy and the DNA fragment, and wherein the at least one marker gene is flanked by nucleotide sequences that are recognized by a specific resolvase, preferably the nucleotide sequences are *res*; even more preferably the at least one marker gene is excised from the chromosome by the action of a resolvase 25 enzyme subsequent to selecting a host cell that grows under the selective conditions.

The gene of interest may encode an enzyme that is naturally produced by the host cell, indeed one may simply want to increase the number of copies of a gene endogenous to 30 the host cell.

Accordingly a preferred embodiment of the invention relates to the method of the first aspect, wherein the gene of interest originates from the host cell.



In another preferred embodiment the invention relates to the method of the first aspect, wherein the gene of interest encodes an enzyme, preferably an amylolytic enzyme, a lipolytic enzyme, a proteolytic enzyme, a cellulytic enzyme, 5 an oxidoreductase or a plant cell-wall degrading enzyme, and more preferably an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, 10 deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, 15 protease, ribonuclease, transferase, transglutaminase, or xylanase.

As mentioned above, the gene of interest may be endogenous to the host cell, however it may be advantageous if the production cell obtained by the method of the invention 20 contains as little exogenous, foreign, or heterologous DNA as possible when the integration procedure is completed.

Consequently a preferred embodiment of the invention relates to the method of the first aspect, wherein the selected host cell that grows under the selective conditions 25 comprises substantially no exogenous DNA, preferably less than 500 basepairs per integrated gene of interest, more preferably less than 300 bp, even more preferably less than 100 bp, still more preferably less than 50 bp, more preferably less than 25 bp per integrated gene of interest, or most preferably no 30 exogenous DNA.

Yet a preferred embodiment of the invention relates to the method of the first aspect, wherein the selected host cell that grows under the selective conditions comprises DNA only of endogenous origin.

Another embodiment relates to the method, wherein the host cell selected in step e) of the first aspect comprises DNA only of endogenous origin.

Many ways exist in the art of rendering a gene non-  
5 functional by alteration or manipulation, such as partially deleting the gene or the promoter of the gene, or by introducing mutations in the gene or the promoter region of the gene.

A preferred embodiment of the invention relates to the  
10 method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell is altered by partially deleting the gene(s), or by introducing one or more mutations in the gene(s).

The present invention relies on rendering at least one  
15 conditionally essential chromosomal gene(s) in the host cell non-functional in a step, and in particular relies on a number of conditionally essential genes to be rendered non-functional. The gene(s) may be rendered non-functional by a partial deletion or a mutation as known in the art;  
20 specifically the gene(s) may be rendered non-functional through the use of a "Deletion plasmid(s)" as shown herein in non-limiting examples below. For each of the preferred embodiments relating to the altered chromosomal gene(s) of step b) of the method of the first aspect, the most preferred  
25 embodiment is shown by non-limiting examples herein and reference is made to the genetic tools constructed for that purpose, such as the PCR primer sequences used for constructing the "Deletion plasmid(s)".

Accordingly a preferred embodiment of the invention relates to  
30 the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered encodes a D-alanine racemase, preferably the gene(s) is a *dal* homologue from a *Bacillus* cell, more preferably the gene is

homologous to *dal* from *Bacillus subtilis*, and most preferably the gene(s) is the *dal* gene of *Bacillus licheniformis*.

Another preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally  
5 essential chromosomal gene(s) of the host cell that is altered encodes a D-alanine racemase and is at least 75% identical, preferably 80% identical, or preferably 85% identical, more preferably 90% identical, or more preferably 95% and most preferably at least 97% identical to the *dal* sequence of  
10 *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12.

The conditionally essential gene(s) may encode polypeptides involved in the utilization of specific carbon sources such as xylose or arabinose, in which case the host  
15 cell is unable to grow in a minimal medium supplemented with only that specific carbon source when the gene(s) are non-functional.

A preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally  
20 essential chromosomal gene(s) of the host cell that is altered is one or more genes that are required for the host cell to grow on minimal medium supplemented with only one specific main carbon-source.

A preferred embodiment of the invention relates to the  
25 method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is of a xylose operon, preferably the gene(s) is homologous to the *xylA* gene from *Bacillus subtilis*, and most preferably the gene(s) is homologous to one or more genes of the xylose  
30 isomerase operon of *Bacillus licheniformis*.

A preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered encodes a galactokinase (EC 2.7.1.6), an UTP-dependent

pyrophosphorylase (EC 2.7.7.10), an UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3), preferably the gene(s) encodes an UDP-galactose epimerase (EC 5.1.2.3), more preferably the gene(s)  
5 is homologous to *galE* of a *Bacillus*, and most preferably the gene is *galE* of *Bacillus licheniformis*.

A preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered  
10 is one or more gene(s) of a gluconate operon, preferably the gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both, more preferably the gene(s) is one or more genes homologous to the *gntK* or *gntP* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *gntK*  
15 or *gntP* gene from *Bacillus licheniformis*.

Another preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of a gluconate operon, preferably the  
20 gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to any of the *gntK* and *gntP* sequences of *Bacillus licheniformis*.

25 Another preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a  
30 glycerol kinase, or a glycerol dehydrogenase, more preferably the gene(s) is one or more genes homologous to the *glpP*, *glpF*, *glpK*, and *glpD* genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *glpP*, *glpF*,

*glpK*, and *glpD* genes from *Bacillus licheniformis* shown in SEQ ID No:26.

Still another preferred embodiment of the invention relates to the method of the first aspect, wherein the  
5 conditionally essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, and is at least 75% identical, preferably 85% identical, more  
10 preferably 95% and most preferably at least 97% identical to any of the *glpP*, *glpF*, *glpK*, and *glpD* sequences of *Bacillus licheniformis* shown in SEQ ID No:26.

One preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally  
15 essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, more preferably the gene(s) is homologous to the *araA* gene from *Bacillus subtilis*, and most preferably the gene(s) is the *araA* gene from *Bacillus*  
20 *licheniformis* shown in SEQ ID No:38.

A preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of an arabinose operon, preferably the  
25 gene(s) encodes an arabinose isomerase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *araA* sequence of *Bacillus licheniformis* shown in SEQ ID No:38.

Other conditionally essential genes are well-described in  
30 the literature, for instance genes that are required for a cell to synthesize one or more amino acids, where a non-functional gene encoding a polypeptide required for synthesis of an amino acid renders the cell auxotrophic for that amino acid, and the cell can only grow if the amino acid is supplied

to the growth medium. Restoration of the functionality of such a gene allows the cell to synthesise the amino acid on its own, and it becomes selectable against a background of auxotrophic cells.

5       Consequently, a preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell encodes one or more polypeptide(s) involved in amino acid synthesis, and the non-functionality of the gene(s) renders  
10 the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s).

A particularly preferred embodiment of the invention relates to the method of the first aspect, wherein the  
15 conditionally essential chromosomal gene(s) of the host cell encodes one or more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *metC* or the  
20 *lysA* gene from *Bacillus licheniformis*.

Another particularly preferred embodiment of the invention relates to the method of the first aspect, wherein the conditionally essential chromosomal gene(s) of the host cell is at least 75% identical, preferably 85% identical, more  
25 preferably 95% identical and most preferably at least 97% identical to the *metC* sequence of *Bacillus licheniformis* shown in SEQ ID No:42 or the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

As described herein the method of the invention is very  
30 relevant for the biotech industry and a number of preferred organisms are very well known in this industry, especially Gram positive host cells, and certainly host cells of the *Bacillus* genus, specifically *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*,

*Bacillus clausii*, *Bacillus coagulans*, *Bacillus lautus*,  
*Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*,  
*Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus*  
*thuringiensis*.

5 A preferred embodiment of the invention relates to the  
method of the first aspect, wherein the host cell is a Gram-  
positive bacterial cell, preferably a *Bacillus* cell, and most  
preferably a *Bacillus* cell chosen from the group consisting of  
*Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus*  
10 *brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus*  
*coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus*  
*licheniformis*, *Bacillus megaterium*, *Bacillus*  
*stearothermophilus*, *Bacillus subtilis*, and *Bacillus*  
*thuringiensis*.

15 Another preferred embodiment of the invention relates to  
the method of the first aspect, wherein the DNA construct is a  
plasmid.

As described elsewhere herein, the present invention  
provides genetic tools for carrying out the method of the  
20 invention, such as host cells, and DNA constructs of the  
invention, such as a DNA construct of the second aspect  
comprising:

- i) an altered non-functional copy of a conditionally  
essential chromosomal gene(s) from a host cell, preferably  
25 the copy is partially deleted; and
- ii) at least one copy of a gene of interest flanked on one  
side by i) and on the other side by a DNA fragment  
homologous to a host cell DNA sequence located on the host  
cell chromosome adjacent to the conditionally essential  
30 gene(s) of i).

A preferred embodiment of the invention relates to the  
DNA construct of the second aspect, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered  
in i) encodes a D-alanine racemase, preferably the gene(s) is

a *dal* homologue from a *Bacillus* cell, more preferably the gene is homologous to *dal* from *Bacillus subtilis*, and most preferably the gene is the *dal* gene of *Bacillus licheniformis*.

Another preferred embodiment of the invention relates to  
5 the DNA construct of the second aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered in i) encodes a D-alanine racemase and is at least 75% identical, preferably 80% identical, or preferably 85% identical, more preferably 90% identical, or more  
10 preferably 95% and most preferably at least 97% identical to the *dal* sequence of *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12.

Yet another preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the altered  
15 non-functional copy of a conditionally essential chromosomal gene(s) from a host cell is one or more gene(s) that is required for the host cell to grow on minimal medium supplemented with only one specific main carbon-source.

A preferred embodiment of the invention relates to the  
20 DNA construct of the second aspect, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered in i) is one or more genes of a xylose operon, preferably the gene(s) is homologous to the *xylA* gene from *Bacillus subtilis*, and most preferably the gene(s) is homologous to one or more  
25 genes of the xylose isomerase operon of *Bacillus licheniformis*.

Still another preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the chromosomal gene(s) of the host cell that is altered in i)  
30 encodes a galactokinase (EC 2.7.1.6), an UTP-dependent pyrophosphorylase (EC 2.7.7.10), an UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3), preferably the gene(s) encodes an UDP-galactose epimerase (EC 5.1.2.3), more preferably the gene(s)



is homologous to the *galE* gene of *Bacillus subtilis*, and most preferably the gene(s) is the *galE* gene of *Bacillus licheniformis*.

One more preferred embodiment of the invention relates to  
5 the DNA construct of the second aspect, wherein the conditionally essential chromosomal gene(s) is one or more genes of a gluconate operon, preferably the gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both, more preferably the gene(s) is homologous to the *gntK* or  
10 *gntP* genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *gntK* and *gntP* from *Bacillus licheniformis*.

Still another preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the  
15 conditionally essential chromosomal gene(s) is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, more preferably the gene(s) is one or more genes homologous to the *glpP*, *glpF*, *glpK*, and *glpD*  
20 genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *glpP*, *glpF*, *glpK*, and *glpD* genes from *Bacillus licheniformis* shown in SEQ ID No:26.

A particularly preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the  
25 conditionally essential chromosomal gene(s) is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most  
30 preferably at least 97% identical to any of the *glpP*, *glpF*, *glpK*, and *glpD* sequences of *Bacillus licheniformis* shown in SEQ ID No:26.

One more preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the

conditionally essential chromosomal gene(s) is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, more preferably the gene(s) is homologous to the *araA* gene from *Bacillus subtilis*, and most  
5 preferably the gene(s) is the *araA* gene from *Bacillus licheniformis* shown in SEQ ID No:38.

A preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the conditionally essential chromosomal gene(s) is one or more gene(s) of an  
10 arabinose operon, preferably the gene(s) encodes an arabinose isomerase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *araA* sequence of *Bacillus licheniformis* shown in SEQ ID No:38.

15 Yet another preferred embodiment of the invention relates to the DNA construct of the second aspect, wherein the conditionally essential chromosomal gene(s) encodes one or more polypeptide(s) involved in amino acid synthesis, and where and the non-functionality of the gene(s) when present in  
20 a cell with no other functional copy(ies) of the gene(s) renders the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s); preferably the conditionally essential chromosomal gene(s)  
25 encodes one or more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *metC* or the *lysA* gene from *Bacillus licheniformis*. Still more preferably  
30 the conditionally essential chromosomal gene(s) is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *metC* sequence of *Bacillus licheniformis* shown in SEQ ID No:42 or

the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

The present invention provides a method for constructing a production host cell that is very useful to the biotech  
5 industry, such as a host cell of the third aspect comprising at least two copies of a gene of interest stably integrated into the chromosome, where at least one copy is integrated adjacent to a conditionally essential *locus* and wherein the cell is obtainable by any of the methods defined in the first  
10 aspects.

The method of the first aspect describes the integration of a gene of interest into the chromosome of a host cell, so that the gene of interest is integrated in a position that is adjacent to the conditionally essential *locus*. The exact  
15 relative positions of the gene of interest and the *locus* are not of major relevance for the method, however generally speaking it is of interest to minimize the distance in basepairs separating the two, both to achieve a more stable integration, but also to minimize the integration of  
20 superfluous DNA sequence into the host cell genome.

Accordingly a preferred embodiment of the invention relates to the host cell of the third aspect, wherein the gene of interest is separated from the conditionally essential *locus* by no more than 1000 basepairs, preferably no more than  
25 750 basepairs, more preferably no more than 500 basepairs, even more preferably no more than 250 basepairs, and most preferably no more than 100 basepairs.

As mentioned above, it is of interest to minimize the presence of integrated or superfluous DNA sequence in the host  
30 cell genome, especially DNA of exogenous origin, and the ideal host cell contains only DNA of endogenous origin such as multiple copies of an endogenous gene of interest integrated in different well defined chromosomal locations.

Consequently a preferred embodiment of the invention relates to the host cell of the third aspect, which contains substantially no exogenous DNA, preferably less than 500 basepairs per integrated gene of interest, more preferably 5 less than 300 bp, even more preferably less than 100 bp, still more preferably less than 50 bp, more preferably less than 25 bp per integrated gene of interest, or most preferably no exogenous DNA.

Another preferred embodiment of the invention relates to 10 the host cell of the third aspect, which contains only endogenous DNA.

Certain bacterial strains are preferred as host cells in the biotech industry as mentioned previously.

A preferred embodiment of the invention relates to the 15 host cell of the third aspect, which is a Gram-positive bacterial cell, preferably a *Bacillus* cell, and most preferably a *Bacillus* cell chosen from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus* 20 *coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*.

Another preferred embodiment of the invention relates to 25 the host cell of the third aspect, wherein a copy of the gene of interest is integrated adjacent to a gene encoding a D-alanine racemase, preferably a gene homologous to the *dal* gene from *Bacillus subtilis*, more preferably a gene at least 75% identical to the *dal* sequence of *Bacillus licheniformis* shown 30 in positions 1303 to 2469 in SEQ ID 12, even more preferably 80% identical, or even more preferably a gene at least 85% identical, still more preferably 90% identical, more preferably at least 95% identical, and most preferably at

least 97% identical to the *dal* sequence of *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12.

A particularly preferred embodiment of the invention relates to the host cell of the third aspect, wherein a copy  
5 of the gene of interest is integrated adjacent to a gene that is required for the host cell to grow on minimal medium supplemented with only one specific main carbon-source.

Yet another preferred embodiment of the invention relates to the host cell of the third aspect, wherein a copy of the  
10 gene of interest is integrated adjacent to a gene of a xylose operon, preferably adjacent to genes homologous to the *xylR* or *xylA* genes from *Bacillus subtilis*, and most preferably adjacent to *xylR* or *xylA* from *Bacillus licheniformis*.

One more preferred embodiment of the invention relates to  
15 the host cell of the third aspect, wherein a copy of the gene of interest is integrated adjacent to a gene encoding a galactokinase (EC 2.7.1.6), an UTP-dependent pyrophosphorylase (EC 2.7.7.10), an UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3),  
20 preferably adjacent to a gene encoding an UDP-galactose epimerase (EC 5.1.2.3), more preferably adjacent to a gene homologous to the *galE* gene from *Bacillus subtilis*, and most preferably adjacent to *galE* from *Bacillus licheniformis*.

An additional preferred embodiment of the invention  
25 relates to the host cell of the third aspect, wherein a copy of the gene of interest is integrated adjacent to a gene of a gluconate operon, preferably adjacent to a gene that encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease, more preferably adjacent to a gene homologous to a *Bacillus*  
30 *subtilis* gene chosen from the group consisting of *gntR*, *gntK*, *gntP*, and *gntZ*, and most preferably adjacent to *gntR*, *gntK*, *gntP*, or *gntZ* from *Bacillus licheniformis*.

Yet an additional preferred embodiment of the invention relates to the host cell of the third aspect, wherein a copy

of the gene of interest is integrated adjacent to a gene of a glycerol operon, preferably the gene encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, more preferably the gene is homologous to the  
5 *glpP*, *glpF*, *glpK*, or *glpD* gene from *Bacillus subtilis*, and most preferably the gene is the *glpP*, *glpF*, *glpK*, or *glpD* gene from *Bacillus licheniformis* shown in SEQ ID No:26.

Another particularly preferred embodiment of the invention relates to the host cell of the third aspect,  
10 wherein a copy of the gene of interest is integrated adjacent to a gene of an arabinose operon, preferably the gene encodes an arabinose isomerase, more preferably the gene is homologous to the *araA* gene from *Bacillus subtilis*, and most preferably the gene is the *araA* gene from *Bacillus licheniformis* shown in  
15 SEQ ID No:38.

Still a preferred embodiment of the invention relates to the host cell of the third aspect, wherein a copy of the gene of interest is integrated adjacent to a gene which encodes one or more polypeptide(s) involved in amino acid synthesis, and  
20 the non-functionality of the gene(s) renders the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s); preferably the gene of interest is integrated adjacent to a gene which encodes one  
25 or more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *metC* or the *lysA* gene from *Bacillus licheniformis*. Also preferably the gene of interest  
30 is integrated adjacent to a gene which is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *metC* sequence of *Bacillus licheniformis* shown in SEQ ID No:42 or the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

The host cell of the third aspect is especially interesting for the industrial production of polypeptides such as enzymes.

A preferred embodiment of the invention relates to the host  
5 cell of the third aspect, wherein the gene of interest encodes an enzyme, preferably an amylolytic enzyme, a lipolytic enzyme, a proteolytic enzyme, a cellulytic enzyme, an oxidoreductase or a plant cell-wall degrading enzyme, and more preferably an enzyme selected from the group consisting of  
10 aminopeptidase, amylase, amyloglucosidase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase,  
15 invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Also preferably the gene of interest encodes an antimicrobial peptide,  
20 preferably an anti-fungal peptide or an anti-bacterial peptide; or the gene of interest encodes a peptide with biological activity in the human body, preferably a pharmaceutically active peptide, more preferably insulin/pro-insulin/pre-pro-insulin or variants thereof, growth hormone or  
25 variants thereof, or blood clotting factor VII or VIII or variants thereof.

A further preferred embodiment of the invention relates to the host cell of the third aspect, wherein no antibiotic markers are present.

30 The present invention teaches the construction of host cells that are suitable for use in the method of the first aspect, especially host cells wherein one, two or more conditionally essential genes are rendered non-functional. In non-limiting examples below is shown how the preferred

conditionally essential genes of the invention are rendered non-functional through a partial deletion by using specific Deletion Plasmids of the invention. Specifically the present invention relates to a *Bacillus* cell of the fourth aspect, 5 which is preferably a *Bacillus licheniformis* cell, wherein at least two conditionally essential genes are rendered non-functional, preferably the genes are chosen from the group consisting of *xylA*, *galE*, *gntK*, *gntP*, *glpP*, *glpF*, *glpK*, *glpD*, *araA*, *metC*, *lysA*, and *dal*.

10 The use of such a host cell of the third aspect is likewise envisioned in the method of the first aspect.

Another genetic tool provided by the present invention for the method of the first aspect, is a host cell comprising a DNA construct of the second aspect.

15 A final aspect of the invention relate to a process for producing an enzyme of interest, comprising cultivating a cell of the third aspect under conditions appropriate for producing the enzyme, and optionally purifying the enzyme.

20

## Examples

### Example 1

*Bacillus licheniformis* SJ4671 (WO 99/41358) comprises two 25 stably integrated *amyL* gene copies in its chromosome, inserted in opposite relative orientations in the region of the *B. licheniformis* alpha-amylase gene, *amyL*. The following example describes the insertion into this strain of a third *amyL* gene copy by selectable, directed integration into another defined 30 region of the *B. licheniformis* chromosome resulting in a strain comprising three stable chromosomal copies of the *amyL* gene but which is devoid of foreign DNA.

Xylose isomerase deletion/integration outline (Figure 1)



The sequence of the *Bacillus licheniformis* xylose isomerase region is available in GenBank/EMBL with accession number Z80222.

A plasmid denoted "Deletion plasmid" was constructed by cloning two PCR amplified fragments from the xylose isomerase region on a temperature-sensitive parent plasmid. The PCR fragments were denoted "A" and "B", wherein A comprises the *xylR* promoter and part of the *xylR* gene; and B comprises an internal fragment of *xylA* missing the promoter and the first 70 basepairs of the gene. A spectinomycin resistance gene flanked by resolvase (*res*) sites was introduced between fragments A and B on the plasmid. This spectinomycin resistance gene could later be removed by resolvase-mediated site-specific recombination.

The xylose isomerase deletion was transferred from the Deletion plasmid to the chromosome of a *Bacillus* target strain by double homologous recombination via fragments A and B, mediated by integration and excision of the temperature-sensitive plasmid. The resulting strain was denoted "Deletion strain". This strain is unable to grow on minimal media with xylose as sole carbon source.

An "Integration plasmid" was constructed for insertion of genes into the xylose isomerase region of the Deletion strain. We intended to PCR-amplify a fragment denoted "C" comprising the *xylA* promoter and about 1 kb of the *xylA* gene. However, as later described, only a smaller fragment denoted "D" comprising the *xylA* promoter and the first 250 basepairs of the *xylA* gene was successfully amplified and cloned. The Integration plasmid comprises fragments A and D on a temperature-sensitive vector. An expression cassette was also cloned in the Integration plasmid between fragments A and D.

The temperature-sensitive Integration plasmid was transferred to the *B. licheniformis* Deletion strain and it integrated in the chromosome; subsequent excision of the

temperature sensitive vector was ensured, and "Integration strains" could then be isolated which grow on minimal media with xylose as sole carbon source. Such Integration strains have restored the chromosomal *xylA* gene, by double homologous recombination via fragments A and D. In this process, the expression cassette has been integrated into the chromosome.

#### Plasmid constructs

PCR amplifications were performed with Ready-To-Go PCR Beads from amersham pharmacia biotech as described in the manufacturers instructions, using an annealing temperature of 55°C.

#### Plasmids pSJ5128 and pSJ5129:

The A fragment (*xylR* promoter and part of the *xylR* gene) was amplified from *Bacillus licheniformis* PL1980 chromosomal DNA using primers:

#183235; [*Hind*III ←Z80222 1242-1261→] (SEQ ID 1):

5'-GACTAAGCTTCTGCATAGTGAGAGAAGACG

#183234: [*Eco*RI; *Bgl*II; *Not*I; *Mlu*I; *Sal*I; *Sca*I ←Z80222 2137-2113→] (SEQ ID 2):

5'-

GACTGAATTCAGATCTGCGGCCGCACGCGTGTGACAGTACTGAAATAGAGGAAAAAATAAGTTTTC

The PCR fragment was digested with *Eco*RI and *Hind*III and purified, then ligated to *Eco*RI and *Hind*III digested pUC19. The ligation mixture was transformed by electroporation into *E. coli* SJ2, and transformants were selected for ampicillin resistance (200 µg/ml). The PCR-fragments of three such ampicillin resistant transformants were sequenced and all were

found to be correct. Two clones designated SJ5128 (SJ2/pSJ5128) and SJ5129 (SJ2/pSJ5129) were kept.

Plasmids pSJ5124, pSJ5125:

5 The B fragment (an internal part of *xylA*, missing the promoter and the first 70 basepairs of the coding region), was amplified from *B. licheniformis* PL1980 chromosomal DNA using primers:

10 #183230 [*EcoRI* ←Z80222 3328-3306→] (SEQ ID 3):

5'-GACTGAATTCCGTATCCATTCCTGCGATATGAG

#183227 [*BamHI*; *BglII* ←Z80222 2318-2342→] (SEQ ID 4):

5'-GACTGGATCCAGATCTTATTACAACCCTGATGAATTTGTCG

15

The PCR fragment was digested with *EcoRI* and *BamHI*, and purified, then ligated to *EcoRI* + *BamHI* digested pUC19 and transformed by electroporation into *E. coli* SJ2. Transformants were selected for ampicillin resistance (200 µg/ml). Two clones were correct as confirmed by DNA sequencing, and were kept as SJ5124 (SJ2/pSJ5124) and SJ5125 (SJ2/pSJ5125).

Plasmid pSJ5130:

The C fragment (comprising the *xylA* promoter and about 1 kb of the *xylA* gene) was PCR amplified from *B. licheniformis* PL1980 chromosomal DNA using primers:

#183230 (see above, SEQ ID 3)

30 #183229 [*BamHI*; *BglII*; *NheI*; *ClaI*; *SacII* ←Z80222 2131-2156→] (SEQ ID 5):

5'-

GACTGGATCCAGATCTGCTAGCATCGATCCGCGGCTATTTCCATTGAAAGCGATTAATTG

The PCR fragment was digested with *EcoRI* and *BamHI* and purified, then ligated to *EcoRI* and *BamHI* digested pUC19 and transformed by electroporation, into *E. coli* SJ2.

5 Transformants were selected for ampicillin resistance (200  $\mu\text{g/ml}$ ). One clone, comprising the full-length PCR fragment, was found to have a single basepair deletion in the promoter region, between the -35 and -10 sequences. This transformant was kept as SJ5130 (SJ2/pSJ5130).

10

Plasmid pSJ5131:

This plasmid was constructed as pSJ5130, above, but turned out to contain a 400 basepair PCR fragment only (the D fragment), comprising the *xylA* promoter and the first 250  
15 basepairs of the *xylA* coding sequence. DNA sequencing confirmed that the no sequence errors were present in the fragment. The transformant was kept as SJ5131 (SJ2/pSJ5131).

Plasmids pSJ5197, pSJ5198:

20 These plasmids comprise the A (*xylR*) fragment on a temperature-sensitive, mobilizable vector. They were constructed by ligating the 0.9 kb *BglII-HindIII* fragment from pSJ5129 to the 5.4 kb *BglII-HindIII* fragment from pSJ2739, and transforming *B. subtilis* DN1885 competent cells with the  
25 ligation mix followed by selecting for erythromycin resistance (5  $\mu\text{g/ml}$ ). Two clones were kept, SJ5197 (DN1885/pSJ5197) and SJ5198 (DN1885/pSJ5198).

Plasmids pSJ5211, pSJ5212:

30 These plasmids contain a *res-spc-res* cassette inserted next to the B fragment. They were constructed by ligating the 1.5 kb *BclI-BamHI* fragment from pSJ3358 into the *BglII* site of pSJ5124, and transforming the ligation mix into *E. coli* SJ2 and selecting for ampicillin resistance (200  $\mu\text{g/ml}$ ) and

spectinomycin resistance (120 µg/ml) resistance. Two clones were kept, wherein the *res-spc-res* cassette was inserted in either of the possible orientations, SJ5211 (SJ2/pSJ5211) and SJ5212 (SJ2/pSJ5212).

5

#### **The Deletion plasmid**

##### Plasmid pSJ5218:

This plasmid contains the *res-spc-res* cassette flanked by the A and B fragments. It was constructed by ligating the 2.5 kb *EcoRI*-*Bam*HI fragment from pSJ5211 to the 5.3 kb *EcoRI*-*Bgl*III fragment from pSJ5197, and transforming the ligation mix into *B. subtilis* DN1885 and selecting for erythromycin (5 µg/ml) and spectinomycin resistance (120 µg/ml) resistance at 30°C. One transformant, SJ5218 (DN1885/pSJ5218) was kept.

15

#### **The Integration plasmids**

##### Plasmids pSJ5247, pSJ5248:

These plasmids comprise the short 400 basepairs D fragment (*PxylA-xylA*) as well as the A fragment (*xylR*) on a temperature-sensitive, mobilizable vector. They were made by ligating the 0.4 kb *Bgl*III-*EcoRI* fragment from pSJ5131 to the 5.3 kb *Bgl*III-*EcoRI* fragment from pSJ5197, and transforming the ligation mix into *B. subtilis* DN1885 and selecting for erythromycin resistance (5 µg/ml) at 30°C. Two transformants, SJ5247 (DN1885/pSJ5247) and SJ5248 (DN1885/pSJ5248) were kept.

#### **Construction of strains with chromosomal *xylA* deletions.**

The deletion plasmid pSJ5218 was transformed into competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), transformants were selected for resistance to spectinomycin (120 µg/ml), erythromycin (5 µg/ml) and tetracycline (5 µg/ml) on plates with D-alanine

30

(100  $\mu\text{g/ml}$ ) at 30°C. Two transformants were kept, SJ5219 and SJ5220.

The two-copy *B. licheniformis* alpha-amylase strain SJ4671, described in WO 99/41358 was used as recipient in 5 conjugations.

Donor strains SJ5219 and SJ5220 were grown overnight at 30°C on LBPSG plates (LB plates with phosphate (0.01 M  $\text{K}_3\text{PO}_4$ ), glucose (0.4 %), and starch (0.5 %)) supplemented with D-alanine (100  $\mu\text{g/ml}$ ), spectinomycin (120  $\mu\text{g/ml}$ ), erythromycin 10 (5  $\mu\text{g/ml}$ ) and tetracycline (5  $\mu\text{g/ml}$ ). The recipient strain was grown overnight on LBPSG plates.

An inoculation needle loopful of donor and recipient were mixed on the surface of a LBPSG plate with D-alanine (100  $\mu\text{g/ml}$ ), and incubated at 30°C for 5 hours. This plate was then 15 replicated onto LBPSG with erythromycin (5  $\mu\text{g/ml}$ ) and spectinomycin (120  $\mu\text{g/ml}$ ), and incubation was at 30°C for 2 days. These four conjugations resulted in between 13 and 25 transconjugants.

Tetracycline-sensitive (indicating absence of pBC16) 20 transconjugants were reisolated on LBPSG with erythromycin (5  $\mu\text{g/ml}$ ) and spectinomycin (120  $\mu\text{g/ml}$ ) at 50°C, incubated overnight, and single colonies from the 50°C plates were inoculated into 10 ml TY liquid cultures and incubated with shaking at 26°C for 3 days. Aliquots were then transferred into 25 fresh 10 ml TY cultures and incubation proceeded overnight at 30°C. The cultures were plated on LBPSG with 120  $\mu\text{g/ml}$  spectinomycin, after overnight incubation at 30°C these plates were replica plated onto spectinomycin and erythromycin, respectively, and erythromycin sensitive, spectinomycin 30 resistant isolates were obtained from all strain conjugations.

The following strains, containing the chromosomal *xylA* promoter and the first 70 basepairs of the *xylA* coding sequence replaced by the *res-spc-res* cassette, were kept:

SJ5231: SJ4671 recipient, SJ5219 donor.

SJ5232: SJ4671 recipient, SJ5220 donor.

Strain phenotypes were assayed on TSS minimal medium agar  
5 plates, prepared as follows. 400 ml H<sub>2</sub>O and 10 g agar is  
autoclaved at 121°C for 20 minutes, and allowed to cool to  
60°C. The following sterile solutions are added:

|   |             |
|---|-------------|
| 1 M Tris pH 7.5                             | 25 ml       |
| 10 2 % FeCl <sub>3</sub> .6H <sub>2</sub> O | 1 ml        |
| 2 % trisodium citrate dihydrate             | 1 ml        |
| 1 M K <sub>2</sub> HPO <sub>4</sub>         | 1.25 ml     |
| 10 % MgSO <sub>4</sub> .7H <sub>2</sub> O   | 1 ml        |
| 10 % glutamine                              | 10 ml; and  |
| 15 20 % glucose                             | 12.5 ml; or |
| 15 % xylose                                 | 16.7 ml     |

*Bacillus licheniformis* SJ4671 grows well on both glucose  
and xylose TSS plates, forming brownish coloured colonies.

20 The *xylA* deletion strains SJ5231-SJ5232 grow well on  
glucose TSS plates, but only a very thin, transparent growth  
is formed on the TSS xylose plates, even after prolonged  
incubation. These strains are clearly unable to use xylose as  
the sole carbon source.

25

**Directed and selectable integration into the *xyl* region.**

Integration plasmid pSJ5247 (containing the D and A  
fragments), and as a negative control pSJ5198 (containing only  
30 the A fragment) were transformed into competent cells of the  
*B. subtilis* conjugation donor strain PP289-5 (which contains a  
chromosomal *dal*-deletion, and plasmids pBC16 and pLS20),  
transformants were selected for resistance to erythromycin (5

$\mu\text{g/ml}$ ) and tetracycline ( $5 \mu\text{g/ml}$ ) on plates with D-alanine ( $100 \mu\text{g/ml}$ ) at  $30^\circ\text{C}$ .

Transformants kept were:

5 SJ5255: PP289-5/pSJ5198.

SJ5257: PP289-5/pSJ5248.

Donor strains SJ5255 and SJ5257 were used in conjugations to recipient SJ5231. Selection of transconjugants was on  
10 erythromycin ( $5 \mu\text{g/ml}$ ), at  $30^\circ\text{C}$ . Transconjugants were streaked on TSS plates with xylose, at  $50^\circ\text{C}$ . In parallel, SJ5221 was streaked as a xylose isomerase positive control strain (also at  $50^\circ\text{C}$ ).

After overnight incubation, all strains had formed a very  
15 thin, transparent growth. The control, however, was better growing and colonies were brownish.

After another day of incubation at  $50^\circ\text{C}$ , some brownish colonies were coming up on the background of thin, transparent growth, in transconjugants derived from SJ5257, i.e. the  
20 strain containing the Integration plasmid with the *PxylA-xyIA* fragment (D). These colonies were steadily growing, and further colonies were coming up, during subsequent days of continued incubation at  $50^\circ\text{C}$ .

No brownish colonies (and no further growth than the  
25 thin, transparent growth seen after the first overnight incubation) were observed from transconjugants derived from SJ5255 (the negative control, unable to restore the chromosomal *xyIA* gene).

### 30 Directed integration of an alpha-amylase gene into the *xyl* region.

#### Construction of an *amyL* containing integration plasmid

Plasmids pSJ5291 and pSJ5292 were constructed from the integration vector plasmid pSJ5247 by digestion of this



plasmid with *Bgl*III, and insertion of the 1.9 kb *amy*L containing *Bgl*III-*Bcl*I fragment from pSJ4457 (described in WO 99/41358). The ligation mixture was transformed into *B. subtilis* DN1885 and two transformants were kept as SJ5291 and 5 SJ5292.

Construction of conjugative donor strains, transfer to *B. licheniformis* hosts, and chromosomal integration

Plasmids pSJ5291 and pSJ5292 were transformed into 10 competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), transformants were selected for resistance to erythromycin (5 µg/ml) and tetracycline (5 µg/ml) on plates with D-alanine (100 µg/ml) at 30°C.

15 Transformants kept were SJ5293 (PP289-5/pSJ5291) and SJ5294 (PP289-5/pSJ5292). These two strains were used as donors in conjugations to xylose isomerase deletion strains SJ5231 and SJ5232. Transconjugants were selected on LBPGA plates with erythromycin (5 µg/ml), and one or two 20 tetracyclin-sensitive transconjugants from each conjugation were streaked on a TSS-xylose plate which was incubated at 50°C. After two days incubation, well-growing colonies were inoculated into liquid TY medium (10 ml) without antibiotics, and these cultures were incubated with shaking at 30°C. After 25 overnight incubation, 100 µl from each culture were transferred into new 10 ml TY cultures, and incubation repeated. This procedure was repeated another two times, and in addition the cultures were plated on TSS-xylose plates at 30°C. After about a week, all plates were replicaplanted onto 30 TSS-xylose as well as LBPSG with erythromycin (5 µg/ml). The following day, putative Em-sensitive strains were restreaked on the same plate types.

The following Em sensitive strains, which all grow well on TSS-xylose plates, were kept:

SJ5308 (from conjugation donor SJ5293, host SJ5231)  
SJ5309 (from conjugation donor SJ5293, host SJ5231)  
SJ5310 (from conjugation donor SJ5293, host SJ5232)  
5 SJ5315 (from conjugation donor SJ5294, host SJ5231)

#### Southern analysis.

The two-copy *amyL* strain SJ4671, and strains SJ5308, SJ5309, SJ5310 and SJ5315, were grown overnight in TY-glucose, and chromosomal DNA was extracted. The chromosomal DNA was digested with *Hind*III, fragments separated by agarose gel electrophoresis, transferred to Immobilon-N<sup>o</sup> filters (Millipore<sup>o</sup>) and hybridised to a biotinylated probe based on *Hind*III digested pSJ5292 (using NEBlot Photope Kit and Photope  
15 Detection Kit 6K).

In the two-copy strain, the two *amyL* gene copies reside on a ~10 kb *Hind*III fragment. In addition, an ~2.8 kb fragment is hybridizing, which is due to hybridization to the *xyl* region. In the four strains with insertions of a third *amyL* gene into the xylose gene region, the ~2.8 kb fragment is  
20 missing and has been replaced by a fragment of ~4.6 kb. This is entirely as expected upon integration of the *amyL* gene into the xylose gene region. The ~10 kb fragment due to the two-copy insertion is retained.

25 In conclusion, the southern analysis shows that strains SJ5308, SJ5309, SJ5310 and SJ5315 have a correctly inserted third *amyL* gene copy in their chromosome.

#### Shake flask evaluation.

30 Strains with the *amyL* gene integrated in the xylose isomerase region, as well as several control strains, were inoculated into 100 ml BPX medium in shake flasks and incubated at 37°C with shaking at 300 rpm for 7 days.

50

Alpha-amylase activity in the culture broth was determined by the Phadebas assay:

| Relative alpha-  |          |
|--|----------|
| 5 amylase  |          |
| Strain   | Units/ml |
| SJ4270 (one copy <i>amyL</i> strain)                                   | 100      |
| SJ4671 (two copy <i>amyL</i> strain)                                   | 161      |
| 10 SJ5231 (two copy <i>amyL</i> strain with <i>xylA</i> gene deletion) | 148      |
| SJ5308 (three-copy <i>amyL</i> strain)                                 | 200      |
| SJ5309 (three-copy <i>amyL</i> strain)                                 | 245      |
| 15 SJ5310 (three-copy <i>amyL</i> strain)                              | 200      |
| SJ5315 (three-copy <i>amyL</i> strain)                                 | 200      |

20

Aliquots from each shake flask were plated on amylase indicator plates. All colonies were amylase positive. Four single colonies from each of SJ4671, SJ5309 and SJ5315 were inoculated into fresh BPX shake flasks, which were cultured as above. Alpha-amylase activity in the culture broth was determined by the Phadebas assay:

| Relative alpha-amylase                    |          |
|---|----------|
| Strain                                    | Units/ml |
| 30 SJ4671 (two copy <i>amyL</i> 1 strain) | 100      |
| SJ4671                                    | 102      |
| SJ4671                                    | 88       |
| SJ4671                                    | 84       |

|   |  |            |
|---|--|------------|
|   | <b>SJ5309 (three-copy amyL strain)</b> | <b>149</b> |
|   | <b>SJ5309</b>                          | <b>141</b> |
|   | <b>SJ5309</b>                          | <b>135</b> |
|   | <b>SJ5309</b>                          | <b>149</b> |
| 5 | <b>SJ5315 (three-copy amyL strain)</b> | <b>135</b> |
|   | <b>SJ5315</b>                          | <b>147</b> |
|   | <b>SJ5315</b>                          | <b>159</b> |
|   | <b>SJ5315</b>                          | <b>153</b> |

---

10 Under these shake flask conditions, the three copy *amyL* strains (bold) seem to produce about 50% more alpha-amylase than the two-copy strain.

#### 15 Example 2

A strain of *Bacillus licheniformis* having two stably integrated *amyL* gene copies in its chromosome, inserted in opposite relative orientations in the region of the *B. licheniformis* alpha-amylase gene, *amyL*, has been described in  
 20 WO 99/41358, as SJ4671. A third copy of the *amyL* gene was inserted in *xylRA* as described above

This describes the insertion into this three-copy strain of a fourth *amyL* gene copy by selectable, directed integration into another region of the *B. licheniformis* chromosome.

25

#### **Gluconat deletion/integration outline (Figure 2)**

The sequence region of the *Bacillus licheniformis* gluconate operon comprising the *gntR*, *gntK*, *gntP*, *gntZ* genes for utilization of gluconate is available in Genbank/EMBL with  
 30 accession number D31631. The region can be schematically drawn as shown in figure 2.

A deletion was introduced by cloning, on a temperature-sensitive plasmid, the PCR amplified fragments denoted as "A" (containing part of the *gntK* and part of the *gntP* gene) and

"B" (containing an internal fragment of *gntZ*). As a help in the selection of deletion strains, a kanamycine resistance gene flanked by resolvase sites was introduced between fragments "A" and "B", resulting in the plasmid denoted  
5 "Deletion plasmid" in figure 2. This kanamycine resistance gene could later be removed by resolvase-mediated site-specific recombination, as described in WO 96/23073.

The deletion was transferred to the chromosome of target strains by double homologous recombination via fragments "A"  
10 and "B", mediated by integration and excision of the temperature-sensitive plasmid. The result was the strain, labelled "Deletion strain" in figure 2. This strain is unable to grow on minimal media with gluconate as sole carbon source.

#### 15 Plasmid constructs

To construct an Integration plasmid to be used for gene insertions, the PCR fragment "C" was amplified. This fragment contained an internal fragment of *gntP* of about 1 Kb. The Integration plasmid consists of fragments "B" and "C" on a  
20 temperature-sensitive vector. The expression cassette destined for integration is cloned between "B" and "C". Upon transfer to the *B. licheniformis* Deletion strain and integration and excision of the temperature-sensitive vector, strains could be isolated which grew on minimal media with gluconate as sole  
25 carbon source. Such strains had restored the chromosomal *gntP* gene by double homologous recombination via fragments "B" and "C". In this process, the expression cassette was integrated into the chromosome resulting in the "Integration strain" of figure 2.

30 PCR amplifications were performed with Ready-To-Go PCR Beads from amersham pharmacia biotech as described in the manufacturers instructions, using an annealing temperature of 55°C.

The Deletion Plasmids pMOL1789 and pMOL1790:

The "B" fragment (containing the internal part of the *gntZ*) was amplified from chromosomal DNA from *Bacillus licheniformis* using primers

5

#187338 [*Ava*I ←D31631 4903-4922→] (SEQ ID 6):

5'-TATTTCCCGAGATTCTGTTATCGACTCGCTC

#187339 [*Eag*I ←D31631 5553-5538→] (SEQ ID 7):

10 5'-GTTTTCGGCCGCTGTCCGTTCTGTCTTT

The fragment was digested with *Ava*I + *Eag*I, ligated to *Ava*I + *Eag*I digested pMOL1642, and the ligated plasmid was introduced, by transformation, into *B. subtilis* JA578 selecting for erythromycin resistance (5 µg/ml). The insert on three clones was sequenced, and all found to be correct. MOL1789 (JA578 (*repF*<sup>+</sup>)/pMOL1789) and MOL1790 (JA578/pMOL1790) were kept. The endpoint of the "B" fragment relative to *gntZ* is shown in fig. 2.

20

Plasmids pMOL1820 and pMOL1821:

The "A" fragment (containing part of the *gntK* and part of the *gntP* gene), was amplified from chromosomal DNA of *Bacillus licheniformis* using primers

25

#184733 [←D31631 3738-3712→] (SEQ ID 8):

5'-GTGTGACGGATAAGGCCGCCGTCATTG

#184788 [←D31631 3041-3068→] (SEQ ID 9):

30 5'-CTCTTGTCTCGGAGCCTGCATTTTGGGG

The fragment was digested with *Cla*I + *Eco*RI, ligated to *Eco*RI + *Cla*I digested pMOL1789, and transformed, by

transformation, into *B. subtilis* PL1801 selecting for erythromycin resistance (5 µg/ml). The insert on three clones was sequenced, and all found to be correct. MOL1820 (JA578/pMOL1820) and MOL1821 (JA578/pMOL1821) were kept. The endpoint of the "A" fragment relative to *gntZ* is shown in fig. 2.

The Integration plasmids pMOL1912 and pMOL1913:

These plasmids contain a short C-terminal part of *gntK* and the entire open reading frame of *gntP* (the "C" fragment) on a temperature-sensitive, mobilizable vector. They were made by ligating a 0.9 kb fragment amplified from chromosomal DNA of *Bacillus licheniformis* using primers:

15 #B1656D07 [←D31631 3617-3642→] (SEQ ID 10):

5'-AGCATTATTCTTCGAAGTCGCATTGG

#B1659F03 [*Bgl*III←D31631 4637-4602→] (SEQ ID 11):

5'-TTAAGATCTTTTTTATACAAATAGGCTTAACAATAAAGTAAATCC

20

The fragment was digested with *Bgl*III + *Eco*RI, ligated to *Bgl*III + *Eco*RI digested pMOL1820, and the ligation mixture transformed, by transformation, into *B. subtilis* PL1801 selecting for erythromycin resistance (5 µg/ml). The insert on three clones was sequenced, and all found to be correct. MOL1912 (PL1801/pMOL1789) and MOL1913 (PL1801/pMOL1913) were kept. The endpoint of the "C" fragment relative to *gntZ* is shown in fig. 2.

These plasmids were found to express functional GntP even if they do not have a promoter sequence directly upstream of the *gntP* gene. In order to enable directed integration in the *gntP* region by selecting for growth on gluconate it was

necessary to delete part of the N- terminal sequence of the *gntP* gene on the integration plasmid pMOL1912.

Plasmids pMOL1972 and pMOL1973:

5        These plasmids are Deletion derivatives of pMOL1912 which contain the entire *gntP* gene except for the first 158 bp coding for 53 amino acids of the N-terminal. The plasmid pMOL1912 was digested with *StuI* + *EcoRV* and re-ligated. The ligation mixture was transformed, by competence, into *B.*  
10 *subtilis* PL1801 selecting for erythromycin resistance (5 µg/ml). The deletion was verified by restriction digest. MOL1972 (PL1801/pMOL1972) and MOL1973 (PL1801/pMOL1973) were kept.

      These plasmids do not support growth on TSS gluconate  
15 plates when introduced as free plasmids in a *gntP* deleted background.

**Construction of strains with chromosomal *gntP* deletions**

      The Deletion plasmid pMOL1920 was transformed into  
20 competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), selecting resistance to kanamycine (10 µg/ml), erythromycin (5 µg/ml) and tetracycline (5 µg/ml) on plates with D-alanine (100 µg/ml) at 30°C. Two transformants  
25 were kept, MOL1822 and MOL1823.

      The two-copy *B. licheniformis* alpha-amylase strain SJ4671, described in WO 99/41358 was used as recipient in conjugations.

      Donor strains MOL1822 and MOL1823 were grown overnight at  
30 30°C on LBPSG plates (LB plates with phosphate (0.01 M K<sub>3</sub>PO<sub>4</sub>), glucose (0.4 %), and starch (0.5 %)) supplemented with D-alanine (100 µg/ml), kanamycine (10 µg/ml), erythromycin (5 µg/ml) and tetracycline (5 µg/ml). The recipient strain was grown overnight on LBPSG plates.



A loopful of donor and recipient were mixed on the surface of a LBPSG plate with D-alanine (100  $\mu\text{g/ml}$ ), and incubated at 30°C for 5 hours. This plate was then replicated onto LBPSG with erythromycin (5  $\mu\text{g/ml}$ ) and kanamycine (10  $\mu\text{g/ml}$ ), and 5 incubation was at 30°C for 2 days. These four conjugations resulted in between 25 and 50 transconjugants.

Tetracycline-sensitive (indicating absence of pBC16) transconjugants were reisolated on LBPSG with erythromycin (5  $\mu\text{g/ml}$ ) and kanamycine (10  $\mu\text{g/ml}$ ) at 50°C, incubated overnight, 10 and single colonies from the 50°C plates were inoculated into 10 ml TY liquid cultures and incubated with shaking at 26°C for 3 days, then aliquots were transferred into fresh 10 ml TY cultures and incubation continued overnight at 30°C. The cultures were then plated on LBPSG with 10  $\mu\text{g/ml}$  kanamycine, 15 after overnight incubation at 30°C these plates were replica plated onto kanamycine and erythromycin, respectively, and erythromycin sensitive, kanamycine resistant isolates were obtained from all strain combinations. The following strains, where part of the *gntP* gene coding for the C-terminal was 20 replaced by the *res-kana-res* cassette, were kept:

MOL1871: SJ4671 recipient, MOL1822 donor.

MOL1872: SJ4671 recipient, MOL1823 donor.

25 Strain phenotypes were assayed on TSS minimal medium agar plates, prepared as follows:

400 ml H<sub>2</sub>O is added 10 g agar and is autoclaved at 121°C for 20 minutes, and allowed to cool to 60°C. The following sterile solutions are added:

30

|  |         |
|--|---------|
| 1 M Tris pH 7.5                          | 25 ml   |
| 2 % FeCl <sub>3</sub> .6H <sub>2</sub> O | 1 ml    |
| 2 % trisodium citrate dihydrate          | 1 ml    |
| 1 M K <sub>2</sub> HPO <sub>4</sub>      | 1.25 ml |

57

|  |             |
|--|-------------|
| 10 % $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ | 1 ml        |
| 10 % glutamine                                 | 10 ml, and  |
| 20 % glucose                                   | 12.5 ml, or |
| 15 % gluconate                                 | 16.7 ml     |

5

*Bacillus licheniformis* SJ4671 grows well on both glucose and gluconate TSS plates, forming brownish coloured colonies. The *gntP* Deletion strains MOL1871 and MOL1872 grow well on glucose TSS plates, but only a very thin, transparent growth is formed on the TSS gluconate plates, even after prolonged incubation. These strains are clearly unable to use gluconate as the sole carbon source.

The same *gntP* deletion procedure is performed on the three copy strain SJ5309 described earlier to prepare for integration of a fourth copy of the amylase expression cassette.

#### Directed and selectable integration into the *gnt* region

Integration plasmid pMOL1972 (containing the "B" and "C" fragments), and as a negative control pMOL1789 (containing only the "B" fragment), were transformed into competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), selecting resistance to erythromycin (5  $\mu\text{g/ml}$ ) and tetracycline (5  $\mu\text{g/ml}$ ) on plates with D-alanine (100  $\mu\text{g/ml}$ ) at 30°C. Transformants kept were:

MOL1974: PP289-5/pMOL1972.

MOL1975: PP289-5/pMOL1973.

30

Donor strains MOL1974 and MOL1975 were used in conjugations to recipient MOL1871 and MOL1872. Selection of transconjugants was on erythromycin (5  $\mu\text{g/ml}$ ), at 30°C. Transconjugants were streaked on TSS plates with gluconate, at

50°C. In parallel, SJ4671 was streaked as a gluconate positive control strain (also at 50°C).

After overnight incubation, all strains had formed a very thin, transparent growth. The control, however, was better  
5 growing and colonies were brownish. After another day of incubation at 50°C, some brownish colonies were coming up on the background of thin, transparent growth, in transconjugants derived from MOL1871 and MOL1872. These colonies were steadily growing, and further colonies appeared, during subsequent days  
10 of continued incubation at 50°C.

No colonies were observed from the *gntP* deleted strains MOL1871 and MOL1872.

#### 15 **Directed integration of an alpha-amylase gene into the *gnt* region**

##### Construction of an *amyL* containing Integration plasmid.

The following is a construction plan for integrating an expression cassette with the alpha-amylase gene in the *gnt* region making use of the selection principle described above.  
20 The integration plasmid pMOL1972 is digested with *Bgl*III, and a 1.9 kb *Bgl*III-*Bcl*I fragment containing *amyL* from pSJ4457 (described in WO 99/41358) is inserted by ligation. The ligation mixture is then transformed into *B. subtilis* DN1885 and transformants selected on LBPSG plates with erythromycin  
25 (5 µg/ml) are verified by restriction digestion of plasmid DNA.

##### Conjugative donor strains, transfer to *B. licheniformis*, and chromosomal integration.

30 The Integration plasmid with the expression cassette is transformed into competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), selecting

resistance to erythromycin (5  $\mu$ g/ml) and tetracycline (5  $\mu$ g/ml) on plates with D-alanine (100  $\mu$ g/ml) at 30°C.

Transformants comprising the Integration plasmid with the expression cassette are preserved and used as donors in 5 conjugations with a *gntP* Deletion recipient of the three-copy strain SJ5309, which in turn was constructed as described for the Deletion strains MOL1871 and MOL1872 described above.

Transconjugants are selected on LBPGA plates with erythromycin (5  $\mu$ g/ml), and one or two tetracyclin-sensitive 10 transconjugants from each conjugation is streaked on a TSS-gluconate plate which is incubated at 50°C. After two days incubation, well-growing colonies are inoculated into liquid TY medium (10 ml) without antibiotics, and these cultures are incubated with shaking at 30°C. After overnight incubation, 100 15  $\mu$ l from each culture is transferred into new 10 ml TY cultures, and incubated. This procedure is repeated twice, and in addition the cultures are plated on TSS-gluconate plates at 30°C.

After about a week, all plates are replica-plated onto 20 TSS-gluconate as well as LBPSG with erythromycin (5  $\mu$ g/ml) and incubated. The following day putative Em-sensitive strains are restreaked on the same plate types

As for integration in the xylose region described earlier, Southern analysis and shake flask evaluation is 25 performed to verify the site of integration in the *gnt* region of the alpha-amylase expression cassette and the increased yield from this four copy strain.

### Example 3

30 *Bacillus licheniformis* SJ4671 (WO 99/41358) comprises two stably integrated *amyL* gene copies in its chromosome, inserted in opposite relative orientations in the region of the *B. licheniformis* alpha-amylase gene, *amyL*. The following example describes the insertion into this strain of a third *amyL* gene

copy by selectable, directed integration into another region of the *B. licheniformis* chromosome.

#### D-alanine racemase deletion/integration outline

- 5       The DNA sequence of the *Bacillus licheniformis* D-alanine racemase region was determined in this work and is shown in positions 1303 to 2469 in SEQ ID 12. A plasmid denoted "Dal-Deletion plasmid" was constructed by cloning one 2281 bp PCR amplified fragment from the D-alanine racemase region of
- 10 *Bacillus licheniformis* on a temperature-sensitive parent plasmid. The PCR 2281 bp fragment was denoted "A", wherein A comprises the sequence from 245 basepairs upstream of the ATG start codon of the *dal* gene to 867 basepairs downstream of the *dal* gene.
- 15       A deletion of 586 basepairs of the C-terminal part of the *dal* gene on the cloned fragment A was done resulting in a plasmid containing the fragments "B" and "C" as shown below. A spectinomycin resistance gene flanked by resolvase (*res*) sites was introduced between fragments "B" and "C" on the plasmid.
- 20 This spectinomycin resistance gene could later be removed by resolvase-mediated site-specific recombination.

      The D-alanine racemase deletion was transferred from the Dal-Deletion plasmid to the chromosome of a *Bacillus* target strain by double homologous recombination via fragments "B" and "C", mediated by integration and excision of the

25 temperature-sensitive Dal-Deletion plasmid. The resulting strain was denoted "Dal-Deletion strain". This strain was unable to grow on media without D-alanine.

      An Integration plasmid was constructed for insertion of

30 genes into the D-alanine region of the Deletion strain. We intended to PCR-amplify a fragment denoted "D" comprising 1117 basepairs of the *dal* gene starting from 41 basepairs downstream of the ATG start codon. The promoter region was substituted with the T1 and T2 terminators from the 3'-

terminal sequence of the *Escherichia coli* *rrnB* ribosome RNA operon (EMBL/e09023: basepair 197-295).

The Integration plasmid comprises fragments D and C on a temperature-sensitive vector. An expression cassette destined  
5 for integration was cloned between the fragments D and C. Upon transfer to the *B. licheniformis* deletion strain, integration, and excision of the temperature-sensitive vector, strains could be isolated which grow on media without D-alanine. Such "Integration strains" have restored the chromosomal *dal* gene,  
10 by double homologous recombination via fragments D and C. In this process, the expression cassette was integrated into the chromosome.

#### Plasmid constructs

15 PCR amplifications were performed with Ready-To-Go PCR Beads from amersham pharmacia biotech as described in the manufacturers instructions, using an annealing temperature of 55°C.

#### 20 Plasmids pJA744:

The A fragment (*dal*-region) was amplified from *Bacillus licheniformis* SJ4671 chromosomal DNA using primers:

#148779; [Upstream of a *Sph*I site in the *dal* region] (SEQ ID  
25 14):

5'-GATGAACTTCTGATGGTTGC

#148780: [*Bam*HI < *dal*] (SEQ ID 15):

5'-AAAGGATCCCCCTGACTACATCTGGC

30

The PCR fragment was digested with *Sph*I and *Bam*HI and purified, then ligated to *Sph*I and *Bam*HI digested pPL2438. Transforming *B. subtilis* JA691 (*repF*<sup>+</sup>, *dal*<sup>-</sup>) competent cells with the ligation mix followed by selecting for kanamycin

resistance (10  $\mu$ g/ml). Correct clones could complement the JA691 dal phenotype.

Plasmid pJA770:

5        This plasmid contains a *res-spc-res* cassette inserted between the B and C fragments. It was constructed by ligating the 1.5 kb *Bcl*I-*Bam*HI fragment from pSJ3358 into the *Bcl*I - *Bcl*I sites of pJA744. Transforming *B. subtilis* JA691 competent cells with the ligation mix followed by selecting for  
10 kanamycin resistance (10  $\mu$ g/ml) and spectinomycin resistance (120  $\mu$ g/ml). Orientation of the spectinomycin resistance gene was could be determined by cutting with *Bcl*I and *Bam*HI.

Dal Deletion plasmid

15 Plasmid pJA851:

A fragment (comprising the *ermC* gene and the replication origin of pE194) was PCR amplified from pSJ2739 plasmid DNA using primers:

20 #170046 [*Not*I; < *ermC* gene and the replication origin of pE194>] (SEQ ID 16)

5'-AAAGCGCCGCGAGACTGTGACGGATGAATTGAAAAAGC

#170047 [*Eco*RI; ← *ermC* gene and the replication origin of  
25 pE194→] (SEQ ID 17):

5'-AAAGAATTCGTGAAATCAGCTGGACTAAAAGG

The PCR fragment was digested with *Eco*RI and *Not*I and purified, then ligated to *Eco*RI and *Not*I digested pJA770.  
30 Transforming *B. subtilis* JA691 competent cells with the ligation mix followed by selecting for erythromycin resistance (5  $\mu$ g/ml) and spectinomycin resistance (120  $\mu$ g/ml).

Plasmid PJA748:

A fragment (comprising the *dal* gene without the promotor region) was PCR amplified from *Bacillus licheniformis* SJ4671 DNA using primers:

5

#150506 [*Bam*HI; < *dal* gene] (SEQ ID 18)

5'-AAAGGATCCCGCAAGCAAAGTTGTTTTTCCGC

#150507 [*Kpn*I; <- *dal* gene] (SEQ ID 19):

10

5'-AAAGGTACCGAAAGACATGGGCCGAAATCG

The PCR fragment was digested with *Kpn*I and *Bam*HI and purified, then ligated to *Kpn*I and *Bam*HI digested pPL2438. Transforming *B. subtilis* JA691 competent cells with the ligation mix followed by selecting for kanamycin resistance (10 µg/ml).

Plasmids pJA762:

A fragment (comprising the T<sub>1</sub> and T<sub>2</sub> Terminators from the *E.coli rrnB* terminal sequence EMBL[e09023] from basepair 197 to 295) was PCR amplified from *Escherichia coli* SJ2 DNA using primers:

#158089 [*Kpn*I; < T<sub>1</sub> and T<sub>2</sub> Terminators of *rrnB*] (SEQ ID 20)

25

5'-AAAGGTACCGGTAATGACTCTCTAGCTTGAGG

#158090 [*Cla*I; < T<sub>1</sub> and T<sub>2</sub> Terminators of *rrnB*] (SEQ ID 21):

5'-CAAATCGATCATCACCGAAACGCGGCAGGCAGC

The PCR fragment was digested with *Kpn*I and *Cla*I and purified, then ligated to *Kpn*I and *Cla*I digested pJA748. Transforming *B. subtilis* JA691 competent cells with the ligation mix followed by selecting for kanamycin resistance (10 µg/ml).



Plasmids pJA767:

A fragment (comprising the 0.7kbp DNA sequence downstream of *dal* (DFS)) was PCR amplified from *B. licheniformis* SJ4671 (WO 99/41358) DNA using primers:

#150508 [*Hind*III; < DFS] (SEQ ID 22)

5'-ATTAAGCTTGATATGATTATGAATGGAATGG

10 #150509 [*Nhe*I; < DFS] (SEQ ID 23):

5'-AAAGCTAGCATCCCCCTGACTACATCTGGC

The PCR fragment was digested with *Hind*III and *Nhe*I and purified, then ligated to *Kpn*I and *Cla*I digested pJA762.  
15 Transforming *B. subtilis* JA691 competent cells with the ligation mix followed by selecting for kanamycin resistance (10 µg/ml).

Plasmid pJA776

20 This plasmid contains the *amyL* cassette flanked by the D and C fragments. It was constructed by ligating the 2.8 kb *Hind*III-*Nhe*I fragment from pSJ4457 to the 4.2 kb *Bam*HI-*Hind*III fragment from pJA767, and transforming the ligation mix into *B. subtilis* JA691 competent cells followed by selecting for  
25 kanamycin resistance (10 µg/ml).

**Dal Integration plasmid**Plasmid pJA1020:

30 This plasmid contains the *amyL* cassette flanked by the D and C fragments. Further the plasmid contains the plasmid pE194 replication origin, *repF* and the *Em<sup>r</sup>*-gene. It was constructed by ligating the 2.7kb *Eco*RI-*Nhe*I fragment of pJA776 to the 3.8kb *Eco*RI-*Nhe*I fragment of pJA851, and transforming the ligation mix into *B. subtilis* JA691 competent

cells followed by selecting for erythromycin resistance (5  $\mu\text{g/ml}$ ).

#### 5 Construction of chromosomal *dal* deletions

The Deletion plasmid pJA851 was transformed into competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), and transformants were selected for  
10 resistance to spectinomycin (120  $\mu\text{g/ml}$ ), erythromycin (5  $\mu\text{g/ml}$ ), and tetracycline (5  $\mu\text{g/ml}$ ) on plates with D-alanine (100  $\mu\text{g/ml}$ ) at 30°C. Transformants were kept as JA954 and used as donor in the following conjugation experiments.

The two-copy *amyL* *B. licheniformis* SJ4671 (WO 99/41358)  
15 was used as recipient in the following conjugation experiments.

Donor strain JA954 were grown overnight at 30°C on LBPSG plates (LB plates with phosphate (0.01 M  $\text{K}_3\text{PO}_4$ ), glucose (0.4 %), and starch (0.5 %)) supplemented with D-alanine (100  
20  $\mu\text{g/ml}$ ), spectinomycin (120  $\mu\text{g/ml}$ ), erythromycin (5  $\mu\text{g/ml}$ ) and tetracycline (5  $\mu\text{g/ml}$ ). The recipient strain SJ4671 was grown overnight on LBPSG plates.

Approx. one loop of an inoculation needle of donor and recipient each were mixed on the surface of a LBPSG plate with  
25 D-alanine (100  $\mu\text{g/ml}$ ), and incubated at 30°C for 5 hours. This plate was then replicated onto LBPSG with erythromycin (5  $\mu\text{g/ml}$ ) and spectinomycin (120  $\mu\text{g/ml}$ ), and was incubated at 30°C for 2 days. These four conjugations resulted in 13 - 25 transconjugants.

30 Tetracycline-sensitive (indicating absence of pBC16) transconjugants were reisolated on LBPSG plates with erythromycin (5  $\mu\text{g/ml}$ ) and spectinomycin (120  $\mu\text{g/ml}$ ) at 50°C, and incubated overnight. Single colonies from the 50°C plates were inoculated into 10 ml TY liquid medium with D-alanine

(100 µg/ml) and incubated with shaking at 26°C for 3 days, whereafter aliquots were transferred into fresh 10 ml TY cultures and incubation was continued overnight at 30°C. The cultures were plated on LBPSG with 120 µg/ml spectinomycin and 5 D-alanine (100 µg/ml), after overnight incubation at 30°C these plates were replica plated onto LBPSG with/without D-alanine (100 µg/ml), spectinomycin and erythromycin, respectively.

D-Alanine autotrophic, erythromycin sensitive, and spectinomycin resistant isolates were obtained from all strain 10 combinations. The following strain comprising the chromosomal *dal* promoter and the first 672 basepairs of the *dal* coding sequence replaced by the *res-spc-res* cassette, was kept:

*B. licheniformis* JA967: SJ4671 recipient, JA954 donor.

15

Strain phenotypes were assayed on LBPG with 120µg spectinomycin supplemented with or without D-alanine (100 µg/ml)

*Bacillus licheniformis* SJ4671 grows well on both plates 20 with or without D-alanine. The *dal* deletion strain JA967 growth well on LBPG D-alanine plates, but not on LBPG plates without D-alanine. These strains are clearly unable to grow without adding D-alanine to the media.

25 **The sequence of the *B. licheniformis* *dal*-region (SEQ ID 12):**

The *dal*-region (comprising the *ycdC* gene, a terminator, the *dal* gene and the sequence downstream of *dal* (*DFS*)) was PCR amplified from *Bacillus licheniformis* ATCC14580 chromosomal DNA using the primers:

30

#145507 [ < *ycdC* - *dal* - *DFS* >] (SEQ ID 24):

5'-GCGTACCGTTAAAGTCGAACAGCG

#150509 [*NheI*; < *ycdC* - *dal* - *DFS* >] (SEQ ID 25):

5'-AAAGCTAGCATCCCCCTGACTACATCTGGC

Sequencing of the D-alanine encoding sequence of *Bacillus licheniformis* that is shown in positions 1303-2469 of SEQ ID 5 12 and a subsequent homology search in the public databases revealed that the newly isolated *dal* gene has a sequence identity of only approx. 67% with the *dal* gene of *Bacillus subtilis*, no other D-alanine racemase encoding genes show a higher homolgy to this new *B. licheniformis dal* gene.

10

Conjugative donor strains, transfer to *B. licheniformis*, and chromosomal integration

The Integration plasmid pJA1020 with the expression cassette is transformed into competent cells of the *B. subtilis* conjugation donor strain PP289-5 (which contains a chromosomal *dal*-deletion, and plasmids pBC16 and pLS20), selecting resistance to erythromycin (5 µg/ml) and tetracycline (5 µg/ml) on plates with D-alanine (100 µg/ml) at 30°C.

20 Transformants comprising the Integration plasmid with the expression cassette are preserved and used as donors in conjugations with a *dal* deletion recipient of the two-copy strain JA967

Transconjugants are selected on LBPGA plates with 25 erythromycin (5 µg/ml), and one or two tetracyclin-sensitive transconjugants from each conjugation is streaked on LBPG plate which is incubated at 50°C. After two days incubation, well-growing colonies are inoculated into liquid TY medium (10 ml) without antibiotics, and these cultures are incubated with 30 shaking at 30°C. After overnight incubation, 100 µl from each culture is transferred into new 10 ml TY cultures, and incubated. This procedure is repeated twice, and in addition the cultures are plated on LBPG plates at 30°C.

All plates are replica-plated onto LBPGS, LBPGS with spectinomycin (120 µg/ml) and LBPSG with erythromycin (5 µg/ml) and incubated. The following day putative Spectinomycin- and erythromycin-sensitive strains are  
5 restreaked on the same plate types

As for integration in the xylose region described earlier, Southern analysis and shake flask evaluation is performed to verify the site of integration in the *dal* region of the alpha-amylase expression cassette and the increased  
10 yield from this three copy strain.

#### Example 4

In this work we did a homology study on the *Bacillus subtilis* genome and a particular region of the *B. licheniformis* chromosome (SEQ ID No:26), and we found that the  
15 *B. licheniformis* region contains the genes *glpP*, *glpF*, *glpK* and *glpD*. The size of the analyzed region is 5761 nucleotides, and the DNA sequence is shown in SEQ ID No: 26.

The *glpP* coding region extends from pos. 261 to pos. 818  
20 in SEQ ID No: 26. A search of EMBL and Swiss-prot databases using the blast program revealed the closest homolog to be the *B. subtilis glpP* gene (on the DNA level) and the *B. subtilis* GlpP protein (on the protein level). The identity, on the DNA level, to the *B. subtilis glpP* coding region was 72.4 % in an  
25 alignment constructed using the GAP program in the GCG program package (Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison, Wisc.). The identity of the deduced GlpP protein to the *B. subtilis* GlpP protein was 78.9 %.

The *glpF* coding region extends from pos. 1048 to pos.  
30 1863 in SEQ ID No: 26. A search of EMBL and Swiss-prot databases using the blast algorithm revealed the closest homolog to be the *B. subtilis glpF* gene (on DNA level) and the *B. subtilis* GlpF protein (on the protein level). The identity, on the DNA level, to the *B. subtilis glpF* coding region was

72.8%. The identity of the deduced GlpF protein to the *B. subtilis* GlpF protein was 79.3 %.

The *glpK* coding region extends from pos. 1905 to pos. 3395 in SEQ ID No: 26. A search of EMBL and Swiss-prot  
5 databases using the blast program revealed the closest homolog to be the *B. subtilis glpK* gene (on the DNA level) and the *B. subtilis* GlpK protein (on the protein level). The identity, on the DNA level, to the *B. subtilis glpK* coding region was 75.6 %. The identity of the deduced GlpK protein to the *B.*  
10 *subtilis* GlpK protein was 85.9 %.

The *glpD* coding region extends from pos. 3542 to pos. 5209 in SEQ ID No: 26. A search of EMBL and Swiss-prot  
databases using the blast program revealed the closest homolog to be the *B. subtilis glpD* gene (on the DNA level) and the *B.*  
15 *subtilis* GlpD protein (on the protein level). The identity, on the DNA level, to the *B. subtilis glpD* coding region was 72.9 %. The identity of the deduced GlpD protein to the *B. subtilis* GlpD protein was 81.9 %.

The *B. licheniformis* region in addition contains a part  
20 of the *yhxB* gene, with the coding region starting at pos. 5394 and extending beyond the end of the sequenced fragment shown in SEQ ID No: 26.

#### Use of the *glpD* gene for directed chromosomal integration

25 In analogy with the strategy of the previous examples, segments of the *glpD* gene and the downstream region were PCR amplified from chromosomal DNA of *B. licheniformis*, and combined to provide vectors useful for, in a first step, deletion of the 3' end of the *glpD* gene, and, in a second  
30 step, restoration of the *glpD* gene and the simultaneous insertion of an expression cassette for a gene of interest into the chromosome.

An internal fragment of the *glpD* gene, denoted '*glpD*', was PCR amplified using the two primers below, according to standard PCR protocol also described elsewhere herein.

- 5 (SEQ ID No: 27) 5'-GACTGAATTCGCAATTTGAAGTGAAAATGGTAGC, and  
(SEQ ID No: 28) 5'-GACTGGATCCAGATCTCATCTTTTCGGGAAATC.

The resulting fragment was purified and digested with EcoRI and BamHI, ligated to pUC19 digested with EcoRI and  
10 BamHI, and the ligation mixture transformed into *E. coli* SJ2 with selection for ampicillin resistance (200 µg/ml). A clone with the correct sequence was kept and denoted SJ5767 (SJ2/pSJ5767).

- 15 A fragment of DNA, derived from the *B. licheniformis* chromosome 55 to 555 basepairs downstream of the 3'-end of the *glpD* gene, was amplified using primers:

- (SEQ ID No: 29) 5'-  
20 GACTGAATTCAGATCTGCGGCCGCACGCGTAGTACTCCCGCGTGAGGCTGTCTTG and  
(SEQ ID No: 30) 5'-GACTAAGCTTCAGTTACGCTCAAACACGTACG.

The resulting fragment was purified and digested with EcoRI and HindIII, ligated to pUC19 digested with EcoRI and  
25 HindIII, and the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml). A clone with the correct sequence was kept as SJ5789 (SJ2/pSJ5789).

The internal fragment of the *glpD* gene was then combined  
30 with a spectinomycin resistance gene, flanked by resolvase sites, by excision of a 1.5 kb BclI-BamHI fragment from pSJ3358 and insertion of this into pSJ5767 which had been digested with BglII. The ligation mixture was transformed into *E. coli* SJ2 selecting ampicillin (200 µg/ml) and spectinomycin

(120  $\mu\text{g/ml}$ ) resistance. A clone with the correct sequence was kept and denoted SJ5779 (SJ2/pSJ5779).

To construct the final plasmid for deletion of the 3'-end of *glpD* in the *B. licheniformis* chromosome, pSJ5789 is digested with HindIII and BglII, and the 0.5 kb fragment is ligated to the 5.5 kb HindIII-BglII fragment of pSJ2739. The ligation mixture is transformed into *B. subtilis* DN1885, selecting for erythromycin resistance (5  $\mu\text{g/ml}$ ) at 30°C. The resulting plasmid is digested with EcoRI and BglII, the 4.8 kb fragment is ligated to the 2.4 kb EcoRI-BamHI fragment excised from pSJ5779, and the ligation mixture is transformed into *B. subtilis* DN1885 selecting for erythromycin resistance (5  $\mu\text{g/ml}$ ) and spectinomycin resistance (120  $\mu\text{g/ml}$ ) at 30°C.

The deletion plasmid is transferred into *B. licheniformis* by use of the *B. subtilis* conjugation donor strain PP289-5, as described in previous examples, and the deletion is transferred to the chromosome using essentially the same procedures as described in previous examples.

The resulting *glpD* deletion strain is tested for growth on TSS minimal medium agar plates with glycerol as the sole carbon source.

The integration plasmid was designed to be able to repair the chromosomal *glpD* gene by homologous recombination, and carries a fragment containing the complete 3'-end of the *glpD* gene. It was useful to remove a BglII site present within the *glpD* gene by site-specific mutation designed to retain the amino acid sequence of the GlpD protein. This mutation was introduced by PCR, as follows.

An internal fragment of the *glpD* gene was amplified using primers

SEQ ID No.27 and SEQ ID No.28.



The 3'-end of the *glpD* gene was amplified using primers

(SEQ ID No: 31) 5'-

CCGAGATTTCCCGAAAAGATGAAATTTGGACTTCTGAATCCGGACTG, and

5 (SEQ ID No: 32) 5'-

GACTAAGCTTAGATCTGCTAGCATCGATTGATTATTAACGAAAATTCACC.

The two amplified fragments were mixed, and the mixture used as template for a PCR amplification using primers SEQ ID No:27 and SEQ ID No:32.

The resulting fragment was digested with EcoRI and HindIII, ligated to EcoRI and HindIII digested pUC19, and the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml). A clone with the correct sequence was identified and designated SJ5775 (SJ2/pSJ5775).

To construct the final integration vector plasmid, pSJ5789 is digested with HindIII and BglII, and the 0.5 kb fragment is ligated to the 5.5 kb HindIII-BglII fragment of pSJ2739. The ligation mixture is transformed into *B. subtilis* DN1885, selecting for erythromycin resistance (5 µg/ml) at 30°C. The resulting plasmid is digested with EcoRI and BglII, ligated to the 1.5 kb BglII-EcoRI fragment excised from pSJ5775, and the ligation mixture is transformed into *B. subtilis* DN1885 selecting for erythromycin resistance (5 µg/ml) at 30°C.

This integration vector plasmid has a number of restriction enzyme sites immediately downstream from the 3'-end of the *glpD* gene, into which an expression cassette is inserted.

The resulting integration plasmid is transferred into the *B. licheniformis glpD* deletion strain by use of the *B. subtilis* conjugation donor strain PP289-5, as described in previous examples.

Cells, in which the integration plasmid has integrated into the chromosome via the *glpD* sequences are isolated by their ability to grow on glycerol minimal media plates at 50°C. Such cells are used as a starting point for isolation of a  
5 strain, which by a second recombination event has lost the integrated plasmid, but has retained the repaired version of the *glpD* gene, together with the expression cassette on the chromosome.

The procedure for obtaining such a strain is equivalent  
10 to the procedure described in previous examples used to isolate strains with an expression cassette integrated at the xylose isomerase region of the chromosome.

Use of the *glpFK* genes for directed chromosomal integration.

15 In analogy with the strategy of the previous examples, segments of the *glpF* gene and the upstream *glpP* region were PCR amplified from chromosomal DNA of *B. licheniformis*, and combined to provide vectors useful for, in a first step, deletion of the promoter and 5' end of the *glpF* gene, and, in  
20 a second step, restoration of the promoter and *glpF* gene and the simultaneous insertion of an expression cassette for a gene of interest into the chromosome, upstream of the *glpF* promoter. Deletion of the *glpF* promoter is expected to abolish expression of the *glpF* gene and the downstream *glpK* gene. PCR  
25 amplifications were performed as previously described.

A DNA fragment containing the *glpP* gene was amplified using primers

30 (SEQ ID No: 33) 5'-GACTAAGCTTGTGAAGGAGATGGAACATGAG, and  
(SEQ ID No: 34)

5' -

GACTGGATCCAGATCTGCGGCCGCACGCGTCGACAGTACTATTTTGTAGTTCCAGTATTTTTT  
CC.

The resulting fragment was purified and digested with HindIII and BamHI, ligated to HindIII and BamHI digested pUC19, and the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml). A correct clone kept was SJ5753 (SJ2/pSJ5753).

A DNA fragment containing most of the *glpF* gene, but lacking the first 160 basepairs of the coding sequence, was amplified using primers

10

(SEQ ID No: 35) 5'-GAGCTCTAGATCTTCGGCGGCATCAGCGGAGC, and

(SEQ ID No: 36) 5'-GACTGAATTCCTTTTGCGCAATATGGAC.

The resulting fragment was digested with XbaI and EcoRI, ligated to XbaI and EcoRI digested pUC19, and the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml). A correct clone was kept as SJ5765 (SJ2/pSJ5765).

20 In order to construct a plasmid useful for the deletion of the promoter and 5'-end of the *glpF* gene, the *glpP* containing fragment is excised from pSJ5753 as a HindIII-BglII fragment, the *glpF* fragment is excised from pSJ5765 as a BglII-EcoRI fragment, and these fragments ligated to the HindIII-EcoRI fragment of pSJ2739. The ligation mixture is transformed into *B. subtilis* DN1885, selecting for erythromycin resistance (5 µg/ml) at 30°C.

The resulting plasmid is digested with BglII, and ligated to a 1.5 kb BclI-BamHI fragment from pSJ3358, containing a spectinomycin resistance gene flanked by resolvase recognition sites. The ligation mixture is transformed into *B. subtilis* DN1885 selecting erythromycin resistance (5 µg/ml) and spectinomycin resistance (120 µg/ml) at 30°C.

The deletion plasmid thus constructed is transferred into *B. licheniformis* by use of the *B. subtilis* conjugation donor strain PP289-5, as described in previous examples, and the deletion is transferred to the chromosome using essentially  
5 the same procedures as described in previous examples.

The resulting *glpF* deletion strain is tested for growth on TSS minimal medium agar plates with glycerol as the sole carbon source.

10 The integration plasmid is designed to be able to repair the *glpFK* gene region by homologous recombination, and carries the *glpF* promoter and intact *glpF* gene. This fragment is amplified from chromosomal *B. licheniformis* DNA using primers:  
(SEQ ID No: 36) and

15

(SEQ ID No: 37)

5' -

GAGCTCTAGATCTGCTAGCATCGATCCGCGGTTAAATGTGAAAAATTATTGACAACG.

20 The resulting fragment is digested with XbaI and EcoRI, ligated to pUC19 digested with XbaI and EcoRI, and the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml). The amplified fragment is subsequently excised from this plasmid as a BglII-EcoRI  
25 fragment, which is ligated to the *glpP* containing fragment which is excised from pSJ5753 as a HindIII-BglII fragment, and to the HindIII-EcoRI fragment of pSJ2739. The ligation mixture is transformed into *B. subtilis* DN1885, selecting for erythromycin resistance (5 µg/ml) at 30°C. An expression  
30 cassette of interest is subsequently inserted into the linker region between the end of the *glpP* gene and the *glpF* promoter.

The resulting integration plasmid is transferred into the *B. licheniformis glpF* deletion strain by use of the *B.*

*subtilis* conjugation donor strain PP289-5, as described in previous examples.

Colonies, in which the integration plasmid has integrated into the chromosome via the *glpF* sequences are isolated by  
5 their ability to grow on glycerol minimal media plates at 50°C. Such colonies are used as starting point for isolation of strains, which by a second recombination event has lost the integrated plasmid, but has retained the repaired version of the *glpF* gene, together with the expression cassette.

10 The procedure for obtaining such strains is equivalent to the previously described procedure to isolate strains with an expression cassette integrated at the xylose isomerase region of the chromosome.

15 Sequential use of *glpD* and *glpFK* for chromosomal integration

This procedure envisages use of a strain having both the *glpD* gene deletion, and the *glpF* gene deletion, as the starting strain, and takes advantage of the ability of a strain, which is unable to express the *glpK* gene product, to  
20 grow on minimal media supplemented with glycerol-3-phosphate, whereas the strain deficient in *glpD* is unable to grow on this substrate.

The procedure is then to first introduce the integration plasmid designed to repair the *glpD* gene, and to select for  
25 proper integration using growth on minimal media with glycerol-3-phosphate. This inserts a copy of the expression cassette next to the *glpD* gene.

In a second step, another copy of the expression cassette can be inserted between the *glpP* and *glpF* genes using the  
30 integration vector designed to repair the *glpF* gene, and selecting for proper integration using growth on minimal media with glycerol.

If the two expression cassettes are identical (or strongly homologous, or containing homologous regions), it may

be advantageous to insert these expression cassettes into the vector plasmids in such an orientation, that they in the final strain would be integrated in opposite orientation relative to each other, thus preventing their loss from the strain by homologous recombination under conditions in which there is no selection for growth on glycerol.

#### Example 5

In this work we did a homology study on the *Bacillus subtilis* genome and a second particular region of the *B. licheniformis* chromosome (SEQ ID No: 38), and we found that the region contains the 3'-end of the *abnA* gene, and the 5'-end of the *araA* gene of *B. licheniformis*. The size of the analyzed region is 1500 nucleotides, and the DNA sequence is shown in SEQ ID No: 38.

The 3'-end of the *abnA* coding region extends from position 1 to position 592 in in SEQ ID No: 38. A search of EMBL and Swiss-prot databases using the blast program revealed the closest homolog to be the *B. subtilis abnA* gene (on the DNA level) and the *B. subtilis* AbnA protein (on the protein level). The identity, on the DNA level, to the corresponding *B. subtilis abnA* coding region was 68.9 %. The identity of the deduced AbnA protein fragment to the corresponding *B. subtilis* AbnA protein fragment was 75.8 %.

The 5'-end of the *araA* coding region extends from position 859 to position 1500 in SEQ ID No: 38. A search of EMBL and Swiss-prot databases using the blast program revealed the closest homolog to be the *B. subtilis araA* gene (on the DNA level) and *Bacillus* AraA proteins (on the protein level). The identity, on the DNA level, to the corresponding *B. subtilis araA* coding region was 68.2 %. The identity of the deduced AraA protein fragment to the corresponding *B. subtilis* AraA protein fragment was 62.6 %. The highest identity, scored

in an alignment to a *Bacillus stearothermophilus* AraA protein fragment, was 68.4 %.

Use of the araA gene for directed chromosomal integration

5 In analogy with the strategy of the previous examples, segments of the araA gene and the upstream abnA region were PCR amplified from chromosomal DNA of *B. licheniformis*, and combined to provide vectors useful for, in a first step, deletion of the promoter and 5' end of the araA gene, and, in  
10 a second step, restoration of the promoter and araA gene and the simultaneous insertion of an expression cassette for a gene of interest into the chromosome, upstream of the araA promoter. PCR amplifications were performed as previously described.

15 A fragment of the abnA gene upstream of araA was amplified using primers:

(SEQ ID No: 39) 5'-GACTAAGCTTCATCCGGCGATCAGTTTAATGC, and  
(SEQ ID No: 40)

20 5'-

GACTGAATTCAGATCTGCGGCCGCACGCGTCGACAGTACTATTTTTTTTTTGACAGAT  
TTCAGAAC.

The resulting fragment was digested with HindIII  
25 and EcoRI, ligated to HindIII and EcoRI digested pUC19, the ligation mixture transformed into *E. coli* SJ2 selecting ampicillin resistance (200 µg/ml), and a correct transformant kept as SJ5751 (SJ2/pSJ5751).

A fragment containing an internal part of the araA  
30 gene was amplified using primers:

(SEQ ID No: 41) 5'-GACTGGATCCAGATCTAGTCGAGTACAAAGCGGTGGC,  
and  
(SEQ ID No: 42) 5'-GACTGAATTCGACCAGCCAAGCTGAATCTGC.

The resulting fragment was digested with BamHI and EcoRI, ligated to BamHI and EcoRI digested pUC19, the ligation mixture transformed into *E. coli* SJ2 selecting  
5 ampicillin resistance (200 µg/ml), and a correct transformant kept as SJ5752 (SJ2/pSJ5760).

The *abnA* gene fragment was excised from pSJ5751 as a HindIII-BglII fragment, ligated to the 5.5 kb HindIII-BglII fragment of pSJ2739, and the ligation mixture  
10 transformed into *B. subtilis* DN1885, selecting for erythromycin resistance (5 µg/ml) at 30°C. A transformant kept was SJ5756 (DN1885/pSJ5756).

Plasmid pSJ5760 was digested with BglII, and a 1.5 kb BamHI-BclI fragment from pSJ3358, containing a  
15 spectinomycin resistance gene flanked by resolvase recognition sites, was inserted. A clone was kept as SJ5777 (SJ2/pSJ5777).

The final deletion plasmid was constructed by excision of the *araA-res-spc-res* fragment from pSJ5777 as  
20 a EcoRI-BamHI fragment, and ligation of this to the large EcoRI-BglII fragment of pSJ5756. The ligation mixture was transformed into *B. subtilis* DN1885, selecting erythromycin resistance (5 µg/ml) and spectinomycin resistance (120 µg/ml) at 30°C. A correct transformant  
25 kept was SJ5803 (SJ2/pSJ5803).

The deletion plasmid pSJ5803 is transferred into *B. licheniformis* by use of the *B. subtilis* conjugation donor strain PP289-5, as described in previous examples, and the deletion is transferred to the chromosome using essentially  
30 the same procedures as described in previous examples.

The resulting *araA* deletion strain is tested for growth on TSS minimal medium agar plates with arabinose as the sole carbon source.



An integration vector plasmid is designed to be able to repair the *araA* gene region by homologous recombination, and carries the *araA* promoter and the 5'-end of the *araA* gene in addition to the *abnA* gene fragment of pSJ5756. The *araA* promoter fragment is amplified from chromosomal *B. licheniformis* DNA using primers synthesized based on the sequence given as SEQ ID No: 26. The plasmid is constructed, so that an expression cassette for a gene of interest can be inserted downstream from the *abnA* gene, but upstream of the *araA* promoter.

The resulting integration plasmid is transferred into the *B. licheniformis araA* deletion strain by use of the *B. subtilis* conjugation donor strain PP289-5, as described in previous examples. Colonies, in which the integration plasmid has integrated into the chromosome via the *araA* sequences are isolated by their ability to grow on arabinose minimal media plates at 50°C. Such colonies are used as starting point for isolation of strains, which by a second recombination event has lost the integrated plasmid, but has retained the repaired version of the *araA* gene, together with the expression cassette.

The procedure for obtaining such strains is equivalent to the previously described procedure to isolate strains with an expression cassette integrated at the xylose isomerase region of the chromosome.

#### Example 6

In this work we did a homology study on the *Bacillus subtilis* genome and a third particular region of the *B. licheniformis* chromosome (SEQ ID No:42), and we found that the *B. licheniformis* region contains the 3'-end of the *ispA* gene and the *metC* gene. The size of the analyzed region is 4078 nucleotides, and the DNA sequence is shown in SEQ ID No: 42.

The 3'-end of the *ispA* coding region extends from pos. 1 to pos. 647 in SEQ ID No: 42. A BLAST search of the EMBL and Swiss-prot databases using this particular sequence revealed the closest homologue (on the DNA level) to be the *B. subtilis* *ispA* gene and (on the protein level) the *B. subtilis* IspA protein. The identity, on the DNA level, to the corresponding *B. subtilis* *ispA* coding region was 72.6 % in an alignment constructed using the AlignX™ program in the Vector NTI™ 6.0 program package (Informax™, Inc.). The identity of the deduced IspA protein fragment to the corresponding *B. subtilis* IspA protein fragment was 82.3 %.

The *metC* coding region extends from pos. 1121 to pos. 3406 in SEQ ID No: 42. A BLAST search of EMBL and Swiss-prot databases using this particular sequence revealed the closest homologue to be the *B. subtilis* *metC* gene (on the DNA level) and the *B. subtilis* MetC protein (on the protein level). The identity, on the DNA level, to the *B. subtilis* *metC* coding region was 72.6 %. The identity of the deduced MetC protein to the *B. subtilis* MetC protein was 84.6 %.

20

#### Use of the *metC* gene for directed chromosomal integration

Segments of the *metC* gene and the downstream region were PCR amplified from chromosomal DNA of *B. licheniformis*, and combined to provide a vector useful for deletion of the 3' end of the *metC* gene.

A fragment of DNA, derived from the *B. licheniformis* chromosome, 4 to 671 basepairs downstream of the 3'-end of the *metC* gene, was amplified using primers:

30 (SEQ ID No: 44) 5'-AAAAAACCCGAGTTTCACAAAAAATCCACTACAAACGCCGCC,  
and  
(SEQ ID No: 45) 5'-TTTTTTTAAAGCTTATGCCGCATGTTTCCTTGCTGTTTTTAC.

The resulting fragment was digested with *Ava*I and *Hind*III, ligated to pMOL1887 digested with *Ava*I and *Hind*III, and the ligation mixture transformed into *B. subtilis* PL1801 with selection for erythromycin (5 µg/ml) and kanamycin (10 µg/ml) at 30°C. One clone was kept as CLO57 (PL1801/pCLO57).

An internal fragment of the *metC* gene, derived from the *B. licheniformis* chromosome, 247 to 754 basepairs into the *metC* open reading frame, was amplified using primers:

10 (SEQ ID No: 46) 5'-AAAAAATCGATTTCAGGGATATAAACGATCCG, and  
(SEQ ID No: 47) 5'-  
TTTTTTTTTTCCATCGCACTGGGATATCAGCTCTTCATAAGCATC.

The resulting fragment was digested with *Cla*I and *Bst*XI,  
15 ligated to pCLO57 digested with *Cla*I and *Bst*XI, and the ligation mixture transformed into *B. subtilis* PL1801 with selection for erythromycin (5 µg/ml) and kanamycin (10 µg/ml) at 30°C. One clone was kept as CLO58 (PL1801/pCLO58).

The resulting deletion plasmid pCLO58 has a cassette  
20 consisting of the internal *metC* fragment followed by the kanamycin resistance gene flanked by resolvase sites, which finally is followed by the DNA fragment downstream of the *metC* gene. The deletion plasmid pCLO58 was transferred to the conjugation donor strain PP1060-1, which is isogen to PP289-5  
25 that previously has been described, except that the gene encoding green fluorescent protein (GFP) has been integrated onto the chromosome. The resulting strain CLO71 (PP1060-1/pCLO58) was selected for erythromycin resistance at 30°C. The donor strain CLO71 was mated with the *B. licheniformis*  
30 recipient SJ3047, selecting conjugants for erythromycin resistance and a *dal*<sup>+</sup> phenotype at 30°C.

One conjugant CLO74 was streaked on kanamycine (20 µg/ml) selecting for cells having plasmids integrated into the chromosome. Plating a resulting strain CLO78 onto SMS-glucose

minimal plates revealed that the plasmid had integrated in the internal part of the *metC* gene resulting in a requirement for methionine. CLO78 was used as a starting point for isolation of strains, which by a second recombination event had lost the integrated plasmid, but had retained the deleted version of the *metC* gene.

Such a strain, denoted, CLO80 is appropriate to be used as a recipient for a plasmid carrying a cassette, which can be directed for integration at the *metC* locus essentially as described in previous examples, under conditions selective for an intact *metC* gene.

#### Example 7

In this work we did a homology study on the *Bacillus subtilis* genome and a fourth particular region of the *B. licheniformis* chromosome (SEQ ID No:48), and we found that the *B. licheniformis* region contains the 3'-end of the *spoVAF* gene and the *lysA* gene. The size of the analyzed region is 3952 nucleotides, and the DNA sequence is shown in SEQ ID No: 48.

The 3'-end of the *spoVAF* coding region extends from pos. 1 to pos. 310 in SEQ ID No: 42. The identity, on the DNA level to the *B. subtilis* *spoVAF* coding region was 62.7%. The identity of the deduced SpoVAF protein to the *B. subtilis* SpoVAF protein was 55.2%.

The *lysA* coding region extends from pos. 1048 to pos. 2367 in SEQ ID No: 48. A BLAST search of EMBL and Swiss-prot databases using this particular sequence revealed the closest homologue to be the *B. subtilis* *lysA* gene (on the DNA level) and the *B. subtilis* LysA protein (on the protein level). The identity, on the DNA level, to the *B. subtilis* *lysA* coding region was 73.0 %. The identity of the deduced LysA protein to the *B. subtilis* LysA protein was 82.2 %.

Use of the *lysA* gene for directed chromosomal integration

In analogy with the strategy of the previous examples herein, segments of the *lysA* gene is PCR amplified from chromosomal DNA of *B. licheniformis*, and combined to provide vectors useful for, in a first step, partial deletion of the  
5 *lysA* gene, rendering a cell auxotrophic for lysine, and, in a second step, restoration of the *lysA* gene and the simultaneous insertion of an expression cassette for a gene of interest into the chromosome. Based on the strategies of the previous examples it is well within the skilled persons knowledge to  
10 determine the necessary primers and selective conditions for performing this procedure.

#### General Materials and Methods

In vitro DNA work, transformation of bacterial strains  
15 etc. were performed using standard methods of molecular biology (Maniatis, T., Fritsch, E. F., Sambrook, J. "Molecular Cloning. A laboratory manual". Cold Spring Harbor Laboratories, 1982; Ausubel, F. M., et al. (eds.) "Current Protocols in Molecular Biology". John Wiley and Sons, 1995;  
20 Harwood, C. R., and Cutting, S. M. (eds.) "Molecular Biological Methods for Bacillus". John Wiley and Sons, 1990).

If not otherwise mentioned, enzymes for DNA manipulations were used according to the specifications of the suppliers. Media used (TY, BPX and LB agar) have been described in EP 0  
25 506 780.

Amylase activity was determined with the Phadebas<sup>R</sup> Amylase Test from Pharmacia & Upjohn as described by the supplier.

The use of a resistance gene, e.g. spectinomycin  
30 resistance or kanamycin resistance, flanked by recognition sites for a site specific recombination enzyme (*res* sites recognized by Resolvase from plasmid pAMBeta1) for easy deletion, has been described in US Patent 5,882,888. In the

same patent are described plasmid pSJ3358, and strain B. subtilis PP289-5.

pUC19 is described in Yanisch-Perron, C., Vieira, J., Messing, J. (1985) Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors. Gene 33, 103-119.

pE194 is described in Horinouchi, S., and Weisblum, B. (1982). Nucleotide sequence and functional map of pE194, a plasmid that specifies inducible resistance to macrolide, lincosamide, and streptogramin type B antibiotics. J. Bacteriol., 150, 804-814.

Plasmid pSJ2739 is described in US Patent 6,100,063.

Plasmid pMOL1642 is shown in SEQ ID No:49 and the following table:

15

| Feature           | Basepairs              | Reference                          |
|-------------------|------------------------|------------------------------------|
| res-site          | 5870..6061             | EMBL:AF007787/4852..4951           |
| Kan(R)            | 6241..162              | EMBL:SA110KAR/1390..2151           |
| res-site          | 203..376               | EMBL:AF007787/4852..4951           |
| Promoter<br>PamyQ | 378..396               | EMBL:A00607/67..181                |
| prsa'             | 492..1008              | <i>B.licheniformis</i>             |
| Ery(R)            | 1133..1864<br>(compl.) | EMBL:SAE194/2857..2004             |
| Pre               | 2276..3484             | EMBL:SAE194/join(3150..3728,1..633 |
| repF              | 4113..4709             | EMBL:SAE194/1244..1594             |
| oriT              | 4805..5368             | EMBL:PP110CG/1021..1575            |
| ups prsa          | 5375..5869             | <i>B.licheniformis</i>             |

Strains *Escherichia coli* SJ2 and *Bacillus subtilis* DN1885 are described in Diderichsen, B., Wedsted, U., Hedegaard, L., Jensen, B. R., Sjøholm, C. (1990). Cloning of *aldB*, which

20

encodes acetolactate decarboxylase, an exoenzyme from *Bacillus brevis*. Journal of Bacteriology 172, 4315-4321.

*Bacillus subtilis* PL1801 is the *B. subtilis* DN1885 with disrupted *apr* and *npr* genes.

- 5        *Bacillus licheniformis* PL1980 is a strain of *B. licheniformis*, which was made unable to produce the alkaline protease by insertion of a chloramphenicol resistance gene into the alkaline protease gene.

- Bacillus subtilis* JA578 is a *B. subtilis* 168 *spo*, *amyE*  
10 with a *repF* expression cassette (SEQ ID No:50) inserted downstream of the *dal* gene (EMBL:BSDAL, Accession# M16207) on the chromosome. The *repF* expression cassette shown in SEQ ID No:50 comprises the maltogenic amylase promoter PamyM (position 1-181 in SEQ ID No:50) from *Bacillus*  
15 *Stearothermophilus* (EMBL:BSAMYL02, Accession #M36539), a linker (position 182-211 in SEQ ID No:50) containing the RBS, fused to the the *repF* gene (position 212-808 in SEQ ID No:50) from the plasmid pE194 (EMBL:PPCG2, accession #J01755), with the RepF start-codon in position 212 and Stop-codon in position  
20 809 of SEQ ID No:50.

*Bacillus subtilis* JA691 is *B. subtilis* JA578 *dal*<sup>-</sup>.

**Claims**

1. A method for constructing a cell comprising at least two copies of a gene of interest stably integrated into the chromosome in different positions, the method comprising the 5 steps of:
- a) providing a host cell comprising at least one chromosomal copy of the gene of interest, and comprising one or more conditionally essential chromosomal gene(s) which has been altered to render the gene(s) non-functional;
  - 10 b) providing a DNA construct comprising:
    - i) an altered non-functional copy of the conditionally essential gene(s) of step a); and
    - ii) at least one copy of the gene of interest flanked on one side by i) and on the other side by a DNA fragment 15 homologous to a host cell DNA sequence located on the host cell chromosome adjacent to the gene(s) of step a); wherein a first recombination between the altered copy of i) and the altered chromosomal gene(s) of step a) restores the conditionally essential chromosomal gene(s) 20 to functionality and renders the cell selectable;
  - c) introducing the DNA construct into the host cell and cultivating the cell under selective conditions that require a functional conditionally essential gene(s); and
  - d) selecting a host cell that grows under the selective 25 conditions of the previous step ; wherein the at least one copy of the gene of interest has integrated into the host cell chromosome adjacent to the gene(s) of step a); and optionally
  - e) repeating steps a) to d) at least once using a different 30 chromosomal gene(s) in step a) in each repeat.
2. A method for constructing a cell comprising at least two copies of a gene of interest stably integrated into the



chromosome in different positions, the method comprising the steps of:

- a) providing a host cell comprising at least one chromosomal copy of the gene of interest;
- 5 b) altering a conditionally essential chromosomal gene(s) of the host cell whereby the gene becomes non-functional;
- c) making a DNA construct comprising:
  - i) an altered non-functional copy of the chromosomal gene(s) of step b); and
  - 10 ii) at least one copy of the gene of interest flanked on one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence adjacent to the gene(s) of step b); wherein a first recombination between the altered copy of i) and the altered
  - 15 chromosomal gene(s) of step b) restores the chromosomal gene(s) to functionality and renders the cell selectable;
- d) introducing the DNA construct into the host cell and cultivating the cell under selective conditions that
- 20 require a functional gene(s) of step b); and
- e) selecting a host cell that grows under the selective conditions of step d); wherein the at least one copy of the gene of interest has integrated into the host cell chromosome adjacent to the gene(s) of step b); and
- 25 optionally
- f) repeating steps a) to e) at least once using a different chromosomal gene(s) in step b) in each repeat.

3. The method of claim 1 or 2, wherein subsequent to the step

30 of introducing the DNA construct and cultivating the cell under selective conditions, or subsequent to the step of selecting a host cell, a second recombination takes place between the DNA fragment and the homologous host cell DNA sequence.

4. The method of claim 3, where the DNA construct further comprises at least one marker gene which is located in the construct such that it is recombined out of the chromosome by  
5 the second recombination.

5. The method of claim 4, wherein the at least one marker gene confers resistance to an antibiotic, preferably the antibiotic is chosen from the group consisting of chloramphenicol,  
10 kanamycin, ampicillin, erythromycin, spectinomycin and tetracycline.

6. The method of claims 4 or 5, wherein a host cell is selected which grows under the selective conditions, and which  
15 cell does not contain the at least one marker gene in the chromosome.

7. The method of any of claims 1 - 6, where the DNA construct further comprises at least one marker gene located between the  
20 altered copy and the DNA fragment, and wherein the at least one marker gene is flanked by nucleotide sequences that are recognized by a specific resolvase, preferably the nucleotide sequences are *res*.

25 8. The method of claim 7, wherein the at least one marker gene is excised from the chromosome by the action of a resolvase enzyme subsequent to selecting a host cell that grows under the selective conditions.

30 9. The method of any of claims 1 - 8, wherein the gene of interest originates from the host cell.

10. The method of any of claims 1 - 9, wherein the gene of interest encodes an enzyme, preferably an amylolytic enzyme, a

lipolytic enzyme, a proteolytic enzyme, a cellulytic enzyme, an oxidoreductase or a plant cell-wall degrading enzyme, and more preferably an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, 5 carbohydrazase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, 10 ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase.

15 11. The method of any of claims 1 - 10, wherein the selected host cell that grows under the selective conditions comprises substantially no exogenous DNA, preferably less than 500 basepairs per integrated gene of interest, more preferably less than 300 bp, even more preferably less than 100 bp, still 20 more preferably less than 50 bp, more preferably less than 25 bp per integrated gene of interest, or most preferably no exogenous DNA.

12. The method of any of claims 1 - 10, wherein the selected 25 host cell that grows under the selective conditions comprises DNA only of endogenous origin.

13. The method of any of claims 1 - 12, wherein the conditionally essential chromosomal gene(s) of the host cell 30 is altered by partially deleting the gene(s), or by introducing one or more mutations in the gene(s).

14. The method of any of claims 1 - 13, wherein the conditionally essential chromosomal gene(s) of the host cell

that is altered encodes a D-alanine racemase, preferably the gene(s) is a *dal* homologue from a *Bacillus* cell, more preferably the gene is homologous to *dal* from *Bacillus subtilis*, and most preferably the gene(s) is the *dal* gene of  
5 *Bacillus licheniformis*.

15. The method of any of claims 1 - 13, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered encodes a D-alanine racemase and is at least  
10 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *dal* sequence of *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12.

15 16. The method of any of claims 1 - 13, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is one or more genes that are required for the host cell to grow on minimal medium supplemented with only one specific main carbon-source.

20

17. The method of claim 16, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is of a xylose operon, preferably the gene(s) is homologous to the *xylA* gene from *Bacillus subtilis*, and most preferably the  
25 gene(s) is homologous to one or more genes of the xylose isomerase operon of *Bacillus licheniformis*.

18. The method of claim 16, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered  
30 encodes a galactokinase (EC 2.7.1.6), an UTP-dependent pyrophosphorylase (EC 2.7.7.10), an UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3), preferably the gene(s) encodes an UDP-galactose epimerase (EC 5.1.2.3), more preferably the gene(s)

is homologous to *galE* of a *Bacillus*, and most preferably the gene is *galE* of *Bacillus licheniformis*.

19. The method of claim 16, wherein the conditionally  
5 essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of a gluconate operon, preferably the gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both, more preferably the gene(s) is one or more genes homologous to the *gntK* or *gntP* genes from  
10 *Bacillus subtilis*, and most preferably the gene(s) is the *gntK* or *gntP* gene from *Bacillus licheniformis*.

20. The method of claim 16, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered  
15 is one or more gene(s) of a gluconate operon, preferably the gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to any of the *gntK* and *gntP*  
20 sequences of *Bacillus licheniformis*.

21. The method of claim 16, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of a glycerol operon, preferably the  
25 gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, more preferably the gene(s) is one or more genes homologous to the *glpP*, *glpF*, *glpK*, and *glpD* genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *glpP*, *glpF*,  
30 *glpK*, and *glpD* genes from *Bacillus licheniformis* shown in SEQ ID No:26.

22. The method of claim 16, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered

is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to any of the *glpP*, *glpF*, *glpK*, and *glpD* sequences of *Bacillus licheniformis* shown in SEQ ID No:26.

23. The method of claim 16, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, more preferably the gene(s) is homologous to the *araA* gene from *Bacillus subtilis*, and most preferably the gene(s) is the *araA* gene from *Bacillus licheniformis* shown in SEQ ID No:38.

24. The method of claim 16, wherein the conditionally essential chromosomal gene(s) of the host cell that is altered is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *araA* sequence of *Bacillus licheniformis* shown in SEQ ID No:38.

25. The method of any of claims 1 - 13, wherein the conditionally essential chromosomal gene(s) of the host cell encodes one or more polypeptide(s) involved in amino acid synthesis, and the non-functionality of the gene(s) renders the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s).

26. The method of claim 25, wherein the conditionally essential chromosomal gene(s) of the host cell encodes one or

more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *metC* or the *lysA* gene from  
5 *Bacillus licheniformis*.

27. The method of claim 25, wherein the conditionally essential chromosomal gene(s) of the host cell is at least 75% identical, preferably 85% identical, more preferably 95%  
10 identical and most preferably at least 97% identical to the *metC* sequence of *Bacillus licheniformis* shown in SEQ ID No:42 or the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

15 28. The method of any of claims 1 - 27, wherein the host cell is a Gram-positive bacterial cell, preferably a *Bacillus* cell, and most preferably a *Bacillus* cell chosen from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*,  
20 *Bacillus clausii*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*.

25 29. The method of any of claims 1 - 28, wherein the DNA construct is a plasmid.

30. A DNA construct comprising:

- 30 i) an altered non-functional copy of a conditionally essential chromosomal gene(s) from a host cell, preferably the copy is partially deleted; and
- ii) at least one copy of a gene of interest flanked on one side by i) and on the other side by a DNA fragment homologous to a host cell DNA sequence located on the host

cell chromosome adjacent to the conditionally essential gene(s) of i).

31. The DNA construct of claim 30, wherein the conditionally  
5 essential chromosomal gene(s) of the host cell that is altered  
in i) encodes a D-alanine racemase, preferably the gene(s) is  
a *dal* homologue from a *Bacillus* cell, more preferably the gene  
is homologous to *dal* from *Bacillus subtilis*, and most  
preferably the gene is the *dal* gene of *Bacillus licheniformis*.

10

32. The DNA construct of claim 30, wherein the conditionally  
essential chromosomal gene(s) of the host cell that is altered  
in i) encodes a D-alanine racemase and is at least 75%  
identical, preferably 85% identical, more preferably 95% and  
15 most preferably at least 97% identical to the *dal* sequence of  
*Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ  
ID 12.

33. The DNA construct of claim 30, wherein the altered non-  
20 functional copy of a conditionally essential chromosomal  
gene(s) from a host cell is one or more gene(s) that is  
required for the host cell to grow on minimal medium  
supplemented with only one specific main carbon-source.

25 34. The DNA construct of claim 33, wherein the conditionally  
essential chromosomal gene(s) is one or more genes of a xylose  
operon, preferably the gene(s) is homologous to the *xylA* gene  
from *Bacillus subtilis*, and most preferably the gene(s) is  
homologous to one or more genes of the xylose isomerase operon  
30 of *Bacillus licheniformis*.

35. The DNA construct of claim 33, wherein the conditionally  
essential chromosomal gene(s) encodes a galactokinase (EC  
2.7.1.6), an UTP-dependent pyrophosphorylase (EC 2.7.7.10), an



UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3), preferably the gene(s) encodes an UDP-galactose epimerase (EC 5.1.2.3), more preferably the gene(s) is homologous to the *galE* gene of  
5 *Bacillus subtilis*, and most preferably the gene(s) is the *galE* gene of *Bacillus licheniformis*.

36. The DNA construct of claim 33, wherein the conditionally essential chromosomal gene(s) is one or more genes of a  
10 gluconate operon, preferably the gene(s) encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease or both, more preferably the gene(s) is homologous to the *gntK* or *gntP* genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *gntK* and *gntP* from *Bacillus licheniformis*.

15

37. The DNA construct of claim 33, wherein the conditionally essential chromosomal gene(s) is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a  
20 glycerol dehydrogenase, more preferably the gene(s) is one or more genes homologous to the *glpP*, *glpF*, *glpK*, and *glpD* genes from *Bacillus subtilis*, and most preferably the gene(s) is one or more genes of *glpP*, *glpF*, *glpK*, and *glpD* genes from *Bacillus licheniformis* shown in SEQ ID No:26.

25

38. The DNA construct of claim 33, wherein the conditionally essential chromosomal gene(s) is one or more gene(s) of a glycerol operon, preferably the gene(s) encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a  
30 glycerol dehydrogenase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to any of the *glpP*, *glpF*, *glpK*, and *glpD* sequences of *Bacillus licheniformis* shown in SEQ ID No:26.

39. The DNA construct of claim 33, wherein the conditionally essential chromosomal gene(s) is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, more preferably the gene(s) is homologous to the *araA* gene from *Bacillus subtilis*, and most preferably the gene(s) is the *araA* gene from *Bacillus licheniformis* shown in SEQ ID No:38.

40. The DNA construct of claim 33, wherein the conditionally essential chromosomal gene(s) is one or more gene(s) of an arabinose operon, preferably the gene(s) encodes an arabinose isomerase, and is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *araA* sequence of *Bacillus licheniformis* shown in SEQ ID No:38.

41. The DNA construct of claim 30, wherein the conditionally essential chromosomal gene(s) encodes one or more polypeptide(s) involved in amino acid synthesis, and where and the non-functionality of the gene(s) when present in a cell with no other functional copy(ies) of the gene(s) renders the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s)

42. The DNA construct of claim 41, wherein the conditionally essential chromosomal gene(s) encodes one or more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most preferably the gene(s) is the *metC* or the *lysA* gene from *Bacillus licheniformis*.

43. The DNA construct of claim 41, wherein the conditionally essential chromosomal gene(s) is at least 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *metC* sequence of  
5 *Bacillus licheniformis* shown in SEQ ID No:42 or the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

44. A host cell comprising at least two copies of a gene of interest stably integrated into the chromosome, where at least  
10 one copy is integrated adjacent to a conditionally essential locus and wherein the cell is obtainable by any of the methods defined in claims 1 - 29.

45. The cell of claim 44, wherein the gene of interest is  
15 separated from the conditionally essential locus by no more than 1000 basepairs, preferably no more than 750 basepairs, more preferably no more than 500 basepairs, even more preferably no more than 250 basepairs, and most preferably no more than 100 basepairs.

20

46. The cell of claims 44 or 45, which contains substantially no exogenous DNA, preferably less than 500 basepairs per integrated gene of interest, more preferably less than 300 bp, even more preferably less than 100 bp, still more preferably  
25 less than 50 bp, more preferably less than 25 bp per integrated gene of interest, or most preferably no exogenous DNA.

47. The cell of claims 44 or 45, which contains only  
30 endogenous DNA.

48. The cell of any of claims 44 - 47, which is a Gram-positive bacterial cell, preferably a *Bacillus* cell, and most preferably a *Bacillus* cell chosen from the group consisting of

*Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus*  
5 *stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*.

49. The cell of any of claims 44 - 48, wherein a copy of the gene of interest is integrated adjacent to a gene encoding a  
10 D-alanine racemase, preferably a gene homologous to the *dal* gene from *Bacillus subtilis*, more preferably a gene at least 75% identical to the *dal* sequence of *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12, even more preferably a gene at least 85% identical, more preferably at  
15 least 95% and most preferably at least 97% identical to the *dal* sequence of *Bacillus licheniformis* shown in positions 1303 to 2469 in SEQ ID 12.

50. The cell of any of claims 44 - 49, wherein a copy of the  
20 gene of interest is integrated adjacent to a gene that is required for the host cell to grow on minimal medium supplemented with only one specific main carbon-source.

51. The cell of claim 50, wherein a copy of the gene of  
25 interest is integrated adjacent to a gene of a xylose operon, preferably adjacent to genes homologous to the *xylR* or *xylA* genes from *Bacillus subtilis*, and most preferably adjacent to *xylR* or *xylA* from *Bacillus licheniformis*.

30 52. The cell of claim 50, wherein a copy of the gene of interest is integrated adjacent to a gene encoding a galactokinase (EC 2.7.1.6), an UTP-dependent pyrophosphorylase (EC 2.7.7.10), an UDP-glucose-dependent uridylyltransferase (EC 2.7.7.12), or an UDP-galactose epimerase (EC 5.1.2.3),

preferably adjacent to a gene encoding an UDP-galactose epimerase (EC 5.1.2.3), more preferably adjacent to a gene homologous to the *galE* gene from *Bacillus subtilis*, and most preferably adjacent to *galE* from *Bacillus licheniformis*.

5

53. The cell of claim 50, wherein a copy of the gene of interest is integrated adjacent to a gene of a gluconate operon, preferably adjacent to a gene that encodes a gluconate kinase (EC 2.7.1.12) or a gluconate permease, more preferably  
10 adjacent to a gene homologous to a *Bacillus subtilis* gene chosen from the group consisting of *gntR*, *gntK*, *gntP*, and *gntZ*, and most preferably adjacent to *gntR*, *gntK*, *gntP*, or *gntZ* from *Bacillus licheniformis*.

15 54. The cell of claim 50, wherein a copy of the gene of interest is integrated adjacent to a gene of a glycerol operon, preferably the gene encodes a glycerol uptake facilitator (permease), a glycerol kinase, or a glycerol dehydrogenase, more preferably the gene is homologous to the  
20 *glpP*, *glpF*, *glpK*, or *glpD* gene from *Bacillus subtilis*, and most preferably the gene is the *glpP*, *glpF*, *glpK*, or *glpD* gene from *Bacillus licheniformis* shown in SEQ ID No:26.

55. The cell of claim 50, wherein a copy of the gene of  
25 interest is integrated adjacent to a gene of an arabinose operon, preferably the gene encodes an arabinose isomerase, more preferably the gene is homologous to the *araA* gene from *Bacillus subtilis*, and most preferably the gene is the *araA* gene from *Bacillus licheniformis* shown in SEQ ID No:38.

30

56. The cell of any of claims 44 - 50, wherein a copy of the gene of interest is integrated adjacent to a gene which encodes one or more polypeptide(s) involved in amino acid synthesis, and the non-functionality of the gene(s) renders

the cell auxotrophic for one or more amino acid(s), and wherein restoration of the functionality of the gene(s) renders the cell prototrophic for the amino acid(s).

5 57. The cell of claim 56, wherein a copy of the gene of interest is integrated adjacent to a gene which encodes one or more polypeptide(s) involved in lysine or methionine synthesis, more preferably the gene(s) is homologous to the *metC* or the *lysA* genes from *Bacillus subtilis*, and most  
10 preferably the gene(s) is the *metC* or the *lysA* gene from *Bacillus licheniformis*.

58. The cell of claim 56, wherein a copy of the gene of interest is integrated adjacent to a gene which is at least  
15 75% identical, preferably 85% identical, more preferably 95% and most preferably at least 97% identical to the *metC* sequence of *Bacillus licheniformis* shown in SEQ ID No:42 or the *lysA* sequence of *Bacillus licheniformis* shown in SEQ ID No:48.

20

59. The cell of any of claims 44 - 58, wherein the gene of interest encodes an enzyme, preferably an amylolytic enzyme, a lipolytic enzyme, a proteolytic enzyme, a cellulytic enzyme, an oxidoreductase or a plant cell-wall degrading enzyme, and  
25 more preferably an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-  
30 galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase,

protease, ribonuclease, transferase, transglutaminase, or xylanase.

60. The cell of any of claims 44 - 58, wherein the gene of interest encodes an antimicrobial peptide, preferably an anti-fungal peptide or an anti-bacterial peptide.

61. The cell of any of claims 44 - 58, wherein the gene of interest encodes a peptide with biological activity in the human body, preferably a pharmaceutically active peptide, more preferably insulin/pro-insulin/pre-pro-insulin or variants thereof, growth hormone or variants thereof, or blood clotting factor VII or VIII or variants thereof.

62. The cell of any of claims 44 - 61, wherein no antibiotic markers are present.

63. A *Bacillus licheniformis* cell, wherein at least two conditionally essential genes are rendered non-functional, preferably the genes are chosen from the group consisting of *xylA*, *galE*, *gntK*, *gntP*, *glpP*, *glpF*, *glpK*, *glpD*, *araA*, *metC*, *lysA*, and *dal*.

64. Use of a cell as defined in claim 63 in a method as defined in any of claims 1 - 29.

65. A cell comprising a DNA construct as defined in claims 30 - 43.

66. A process for producing an enzyme of interest, comprising cultivating a cell as defined in any of claims 44 - 62 under conditions appropriate for producing the enzyme, and optionally purifying the enzyme.

1/3

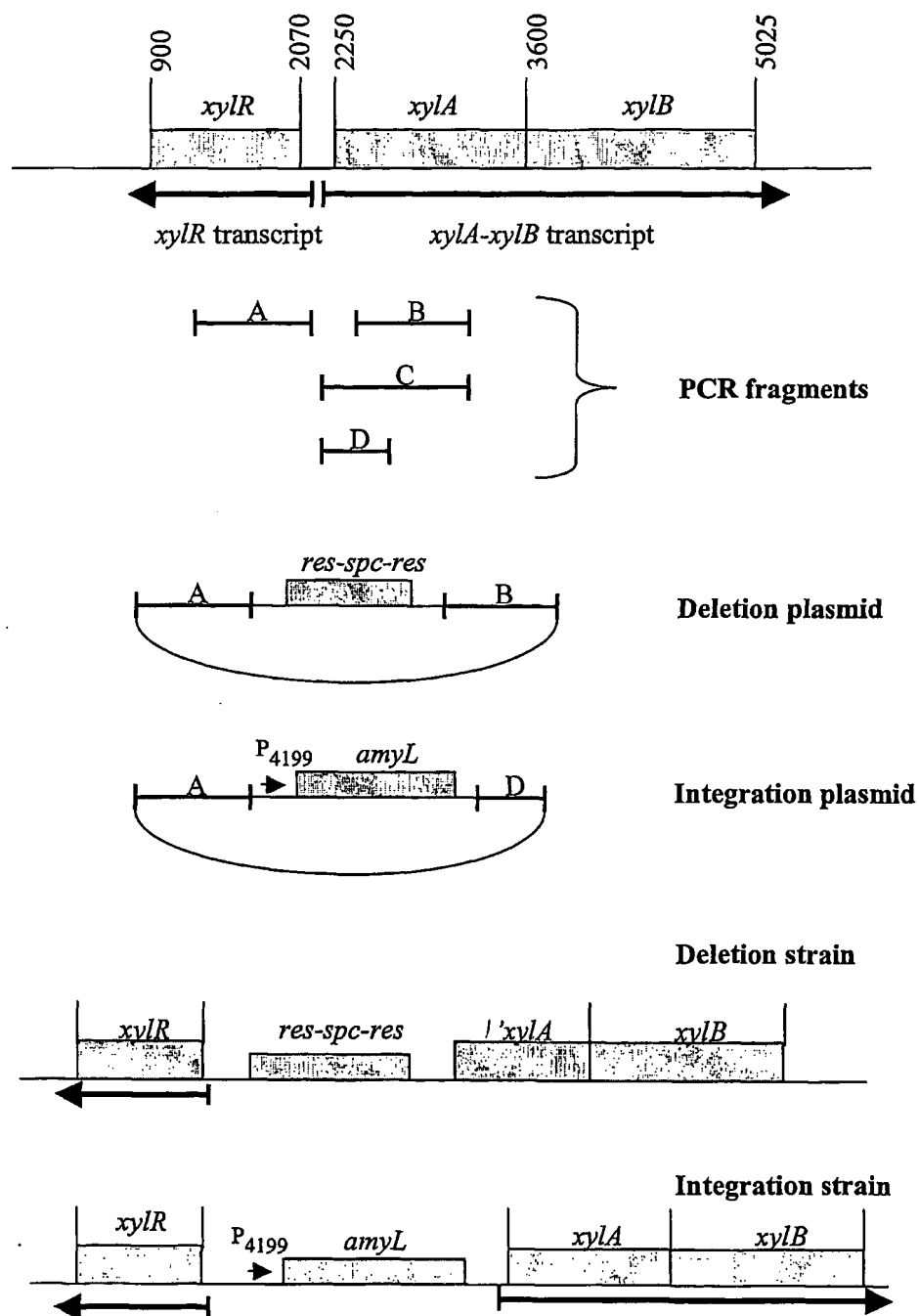


Fig 1



2/3

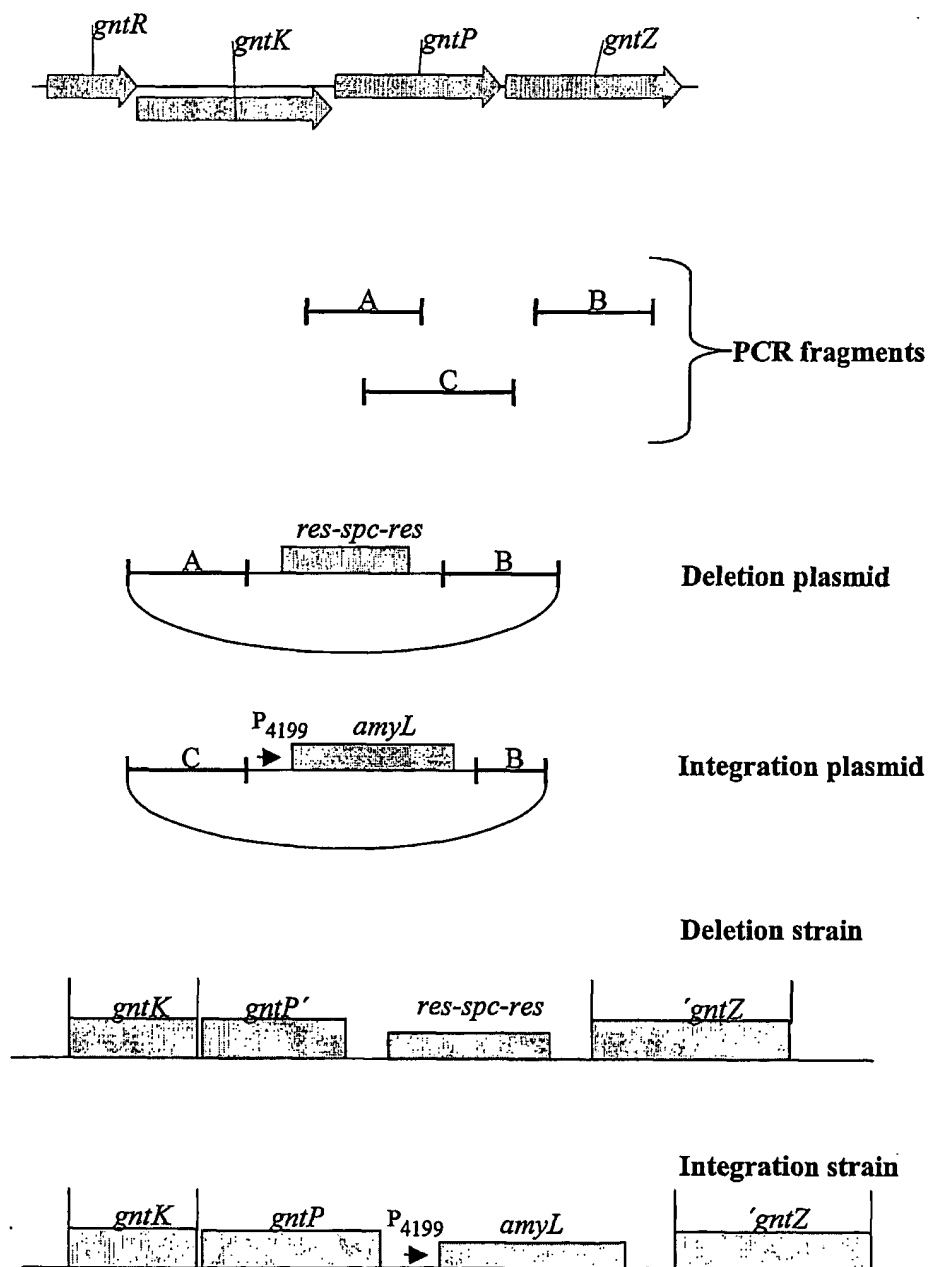


Fig 2

3/3

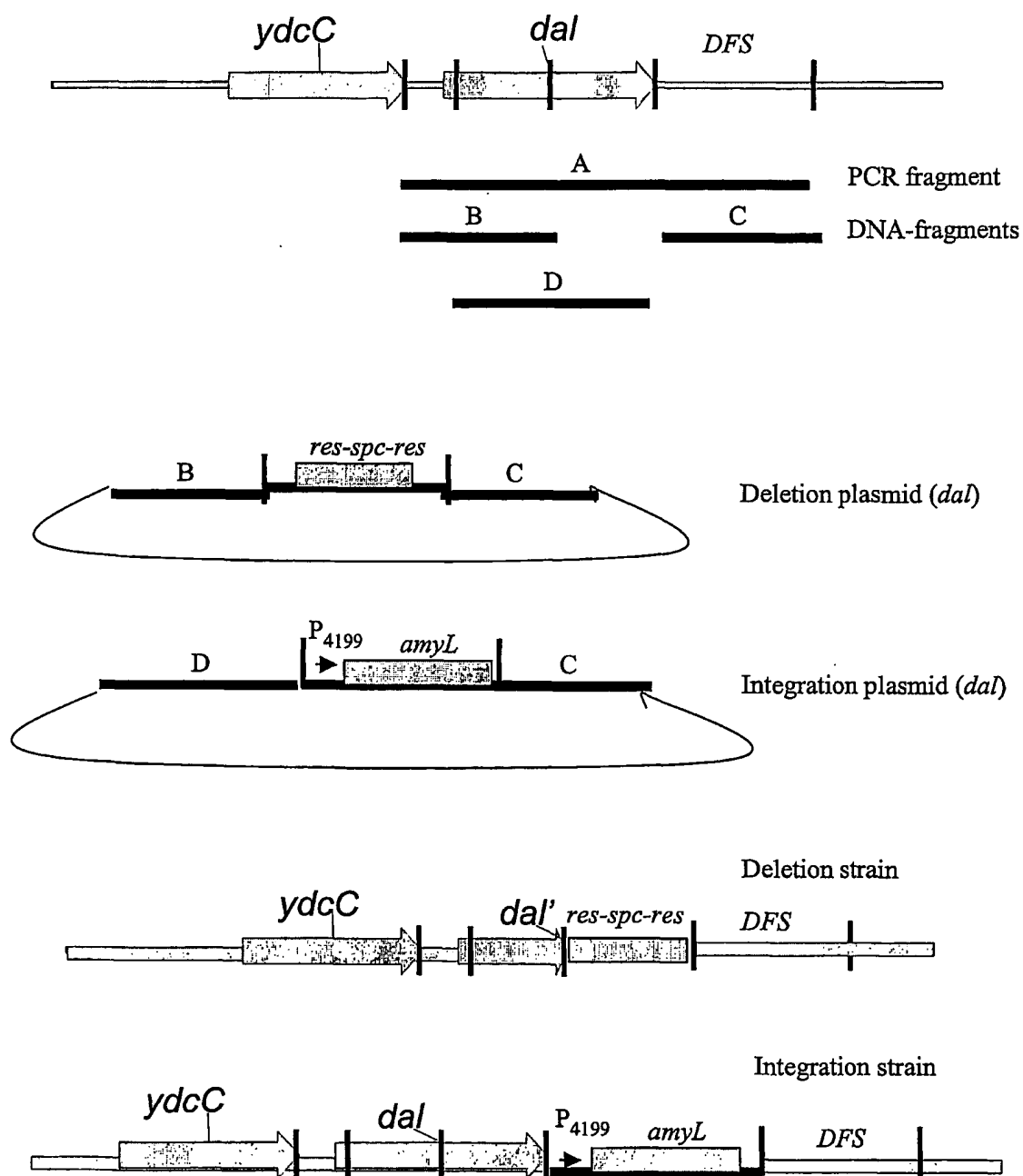


Fig 3

10022.204-WO.ST25  
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<212> DNA  
<213> Artificial Sequence: Primer #183234

30

## 10022.204-WO.ST25

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agtttttc 67

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<211> 33

<212> DNA

<213> Artificial Sequence: Primer #183230

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<211> 41

<212> DNA

<213> Artificial Sequence: Primer #183227

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<213> Artificial Sequence: Primer #183229

<400> 5  
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<212> DNA

<213> Artificial Sequence: Primer #187338

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<210> 7

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<212> DNA

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&lt;213&gt; Artificial Sequence: Primer #187339

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&lt;210&gt; 8

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence:Primer #184733

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&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer #184788

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&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer #B1656D07

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&lt;213&gt; Artificial Sequence: Primer #B1659F03

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&lt;211&gt; 3342

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&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1303)..(2469)

&lt;223&gt; DNA sequence of the dal-gene encoding D-alanine racemase

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2685)..(2685)

&lt;223&gt; Not determined with certainty

&lt;400&gt; 12

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## 10022.204-WO.ST25

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| Met Ser Leu Lys   |      |
| 1   |      |
| cca ttc tat aga aag aca tgg gcc gaa atc gat tta acg gct tta aaa | 1362 |
| Pro Phe Tyr Arg Lys Thr Trp Ala Glu Ile Asp Leu Thr Ala Leu Lys |      |
| 5 10 15 20  |      |
| gaa aac gtc cgc aat atg aag cgg cac atc ggc gag cat gtc cgc ctg | 1410 |
| Glu Asn Val Arg Asn Met Lys Arg His Ile Gly Glu His Val Arg Leu |      |
| 25 30 35  |      |
| atg gcc gtc gtt aaa gcg aat gcc tac gga cac ggg gat gca cag gta | 1458 |
| Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Asp Ala Gln Val |      |
| 40 45 50  |      |
| gcg aag gcg gct ctt gca gaa ggg gcg tcc att ctt gct gtg gct tta | 1506 |
| Ala Lys Ala Ala Leu Ala Glu Gly Ala Ser Ile Leu Ala Val Ala Leu |      |
| 55 60 65  |      |
| ttg gat gaa gcg ctt tcg ctg agg gcg cag ggg att gaa gaa ccg att | 1554 |
| Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile Glu Glu Pro Ile |      |
| 70 75 80  |      |
| ctt gtc ctc ggt gca gtg ccg acc gaa tat gca agc att gcc gcg gaa | 1602 |
| Leu Val Leu Gly Ala Val Pro Thr Glu Tyr Ala Ser Ile Ala Ala Glu |      |
| 85 90 95 100  |      |
| aag cgc att atc gtg act ggc tac tcc gtc ggc tgg ctg aaa gac gtg | 1650 |
| Lys Arg Ile Ile Val Thr Gly Tyr Ser Val Gly Trp Leu Lys Asp Val |      |
| 105 110 115   |      |
| ctc ggt ttt ctg aat gag gcc gaa gct cct ctt gaa tat cat ttg aag | 1698 |
| Leu Gly Phe Leu Asn Glu Ala Glu Ala Pro Leu Glu Tyr His Leu Lys |      |
| 120 125 130   |      |
| atc gac acg ggc atg ggc cgc ctt ggc tgc aaa acg gaa gaa gag atc | 1746 |
| Ile Asp Thr Gly Met Gly Arg Leu Gly Cys Lys Thr Glu Glu Glu Ile |      |
| 135 140 145   |      |
| aaa gaa atg atg gag atg acc gaa tcg aac gat aag ctc aat tgt acg | 1794 |
| Lys Glu Met Met Glu Met Thr Glu Ser Asn Asp Lys Leu Asn Cys Thr |      |
| 150 155 160   |      |
| ggc gtg ttc act cat ttc gcc acg gcg gac gaa aag gac acc gat tat | 1842 |
| Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys Asp Thr Asp Tyr |      |
| 165 170 175 180   |      |
| ttc aac atg cat ctt gac cgc ttt aaa gag ctg atc agc ccc ttc ccg | 1890 |
| Phe Asn Met His Leu Asp Arg Phe Lys Glu Leu Ile Ser Pro Phe Pro |      |
| 185 190 195   |      |
| ctt gac cgt ttg atg gtg cat tcg tca aac agc gcc gcg ggt ctg cgc | 1938 |
| Leu Asp Arg Leu Met Val His Ser Ser Asn Ser Ala Ala Gly Leu Arg |      |
| 200 205 210   |      |
| ttc agg gaa cag cta ttt aat gcc gtc cgc ttc ggc atc ggc atg tac | 1986 |
| Phe Arg Glu Gln Leu Phe Asn Ala Val Arg Phe Gly Ile Gly Met Tyr |      |
| 215 220 225   |      |
| ggt ttg gcg ccg tca acc gaa ata aaa gac gag ctg ccg ttt cgt ctg | 2034 |
| Gly Leu Ala Pro Ser Thr Glu Ile Lys Asp Glu Leu Pro Phe Arg Leu |      |
| 230 235 240   |      |
| cgg gaa gtg ttt tcg ctt cat acc gaa ctc acc cat gtg aaa aaa att | 2082 |
| Arg Glu Val Phe Ser Leu His Thr Glu Leu Thr His Val Lys Lys Ile |      |
| 245 250 255 260   |      |

## 10022.204-wo.ST25

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| gac gaa tgg atc ggg aca gtc ccc gtc ggg tat gcc gac gga tgg ctg<br>Asp Glu Trp Ile Gly Thr Val Pro Val Gly Tyr Ala Asp Gly Trp Leu<br>280 285 290     | 2178 |
| agg cgc ctg gcc gga acg gaa gtg ctg atc gac gga aaa cgc caa aaa<br>Arg Arg Leu Ala Gly Thr Glu Val Leu Ile Asp Gly Lys Arg Gln Lys<br>295 300 305     | 2226 |
| ata gca ggg aga atc tgc atg gac cag ttc atg att tcc ctt gcc gaa<br>Ile Ala Gly Arg Ile Cys Met Asp Gln Phe Met Ile Ser Leu Ala Glu<br>310 315 320     | 2274 |
| gaa tac cct gtc ggc aca aag gtt acc ttg atc gga aag caa aaa gac<br>Glu Tyr Pro Val Gly Thr Lys Val Thr Leu Ile Gly Lys Gln Lys Asp<br>325 330 335 340 | 2322 |
| gaa tgg atc tca gtc gac gaa atc gcc caa aat ttg cag acg atc aat<br>Glu Trp Ile Ser Val Asp Glu Ile Ala Gln Asn Leu Gln Thr Ile Asn<br>345 350 355     | 2370 |
| tat gaa att acc tgt atg ata agt tca agg gtg ccc cgt atg ttt ttg<br>Tyr Glu Ile Thr Cys Met Ile Ser Ser Arg Val Pro Arg Met Phe Leu<br>360 365 370     | 2418 |
| gaa aat ggg agt ata atg gaa ata agg aat ccg atc ttg cct gat caa<br>Glu Asn Gly Ser Ile Met Glu Ile Arg Asn Pro Ile Leu Pro Asp Gln<br>375 380 385     | 2466 |
| tcc tgaaaaattga tgaattagcg gaaaaacaac tttgcttgcg aaaagaataa<br>Ser  | 2519 |
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| gtttttgtct gaatccagcg caacaactga aatattgatt cgcttgccag aagctttagt   | 2639 |
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| ctattgttgc agccataaca gcccaaatc agaaagcaaa attacctacc cacgtcgaaa  | 3059 |
| ttgatgcgaa acgctacggt tttgaaagag actccgttat attgctcgaa caaattcggg   | 3119 |
| cgattgacaa gcaaagatta acggacaaaa tcacccatct cgatgatgaa atgatggaaa   | 3179 |
| aggatcaacga agccttacaa atcagtttgg cactcattga tttttaatat tgatgaaagt  | 3239 |
| tgctcgaggc gaaagagcaa ctttttttgt gttcaaaaat aacaatacga tataatggta   | 3299 |
| actgttagtc ctaaaaatgt tagccagatg tagtcagggg gat   | 3342 |

&lt;210&gt; 13



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&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2685)..(2685)

&lt;223&gt; Not determined with certainty

&lt;400&gt; 13

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His Val Arg Leu Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly  
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Asp Ala Gln Val Ala Lys Ala Ala Leu Ala Glu Gly Ala Ser Ile Leu  
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Ala Val Ala Leu Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile  
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Glu Glu Pro Ile Leu Val Leu Gly Ala Val Pro Thr Glu Tyr Ala Ser  
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Ile Ala Ala Glu Lys Arg Ile Ile Val Thr Gly Tyr Ser Val Gly Trp  
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Leu Lys Asp Val Leu Gly Phe Leu Asn Glu Ala Glu Ala Pro Leu Glu  
 115 120 125

Tyr His Leu Lys Ile Asp Thr Gly Met Gly Arg Leu Gly Cys Lys Thr  
 130 135 140

Glu Glu Glu Ile Lys Glu Met Met Glu Met Thr Glu Ser Asn Asp Lys  
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Leu Asn Cys Thr Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys  
 165 170 175

Asp Thr Asp Tyr Phe Asn Met His Leu Asp Arg Phe Lys Glu Leu Ile  
 180 185 190

Ser Pro Phe Pro Leu Asp Arg Leu Met Val His Ser Ser Asn Ser Ala  
 195 200 205

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Ala Gly Leu Arg Phe Arg Glu Gln Leu Phe Asn Ala Val Arg Phe Gly  
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 225 230 235 240  
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 Val Lys Lys Ile Lys Lys Gly Glu Ser Val Ser Tyr Gly Ala Thr Tyr  
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 325 330 335  
 Lys Gln Lys Asp Glu Trp Ile Ser Val Asp Glu Ile Ala Gln Asn Leu  
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 Arg Met Phe Leu Glu Asn Gly Ser Ile Met Glu Ile Arg Asn Pro Ile  
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 Leu Pro Asp Gln Ser  
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&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 148779

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 26

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 148780

&lt;400&gt; 15

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26

&lt;210&gt; 16

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 170046

&lt;400&gt; 16

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&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 170047

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 150506

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 150507

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&lt;213&gt; Artificial Sequence: Primer # 158089

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&lt;211&gt; 33

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&lt;213&gt; Artificial Sequence: Primer # 158090

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&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 150508

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&lt;213&gt; Artificial Sequence: Primer # 150509

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&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 145507

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&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer # 150509

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&lt;210&gt; 26

&lt;211&gt; 5761

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;400&gt; 26

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| gcaaacctgt | tcagtgaaac | attggggact | tttattctcg  | ttctcggact | tttaacgatc  | 1500 |
| ggtgcaaaca | agtttactga | cggactgaat | cctcttggtg  | tcggatttct | gatcgtggcg  | 1560 |
| atcggtatct | cgctcggcgg | aacaacaggc | tatgcgatta  | accctgcccg | cgatctgggg  | 1620 |
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| gcgtggatcc | ctgttttagg | accggcgctt | ggcggttcat  | ttgcaggcgt | tttttacaac  | 1740 |
| gccgtattca | aagggcatat | cacaaacaca | ttttggattg  | taagcgttat | actagtgtg   | 1800 |
| atattgttag | gtttctatat | tcatatgaaa | aaacaagcag  | ttgatcaatc | ggtcaacatt  | 1860 |
| taaaaaaaa  | caatcttaac | agacatataa | gggggagttt  | caaatggaa  | aagtacattt  | 1920 |
| tgtctcttga | tcaaggcacc | acaagcacia | gggcgattgt  | tttcaacaaa | gcaggcgaaa  | 1980 |
| tcgtccatat | tgcgcaaaag | gaattccagc | aatattttcc  | aaaccccggc | tgggttgaac  | 2040 |
| acaatgcaaa | cgaaatctgg | ggctctgttc | tgtcgggtgat | cgcttcagcg | ctttcagaat  | 2100 |
| cggggatcga | agccggacaa | attgccggaa | tcgggatcac  | aaaccagcgg | gaaacgaccg  | 2160 |
| tggtttggga | taaacatacc | ggcaaaccgg | tctacaacgc  | gattgtgtgg | cagtcccgcc  | 2220 |
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<213> Artificial Sequence: Primer



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10022.204-WO.ST25

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer

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32

&lt;210&gt; 40

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer

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10022.204-WO.ST25

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence: Primer

&lt;400&gt; 45

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&lt;211&gt; 32

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&lt;213&gt; Artificial Sequence: Primer

10022.204-WO.ST25

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| gccatgattc  | agcttgccga  | acaagagggg  | ctgtctctgg | atgtggtatc | gggaggagag  | 1320 |
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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 01/00436

## A. CLASSIFICATION OF SUBJECT MATTER

IPC7: C12N 15/90, C12N 15/68, C12N 15/67 // C12N 15/75  
According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages   | Relevant to claim No. |
|-----------|--|-----------------------|
| A         | WO 9941358 A1 (NOVO NORDISK A/S), 19 August 1999<br>(19.08.99)<br>--                 | 1-66                  |
| A         | EP 0185512 A1 (NOVO INDUSTRI A/S), 25 June 1986<br>(25.06.86)<br>--                  | 1-66                  |
| A         | EP 0972838 A1 (ROCHE DIAGNOSTICS GMBH),<br>19 January 2000 (19.01.00)<br>--<br>----- | 1-66                  |

☐ Further documents are listed in the continuation of Box C. ☒ See patent family annex.

\* Special categories of cited documents:

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

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